

## **FIGURE 1**

GGGGCTCGGCGCCAGCGGCCAGCGCTAGCGGTCTGGTAAGGATTACAAAAGGTGCAGGTATG  
AGCAGGTCTGAAGACTAACATTGTGAAGTTGTAACAGAAAACCTGTTAGAAATGTGGTGGT  
TTCAGCAAGGCCTCAGTTCTTCTTGAGCCCTTGTAAATTGGACATCTGCTGCTTTCATATT  
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGTTACCTTATATCAGTGACACTGG  
TACAGTAGCTCCAGAAAAATGCTTATTGGGCAATGCTAAATATTGCGGCAGTTATGCAATTG  
CTACCATTATGTTGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAA  
TTAAACAAGGCTGGCCTTGTACTTGAATACTGAGTTGTTAGGACTTCTATTGTCATGGCAAACCTT  
CCAGAAAACAACCCTTTTGCTGCACATGTAAGTGGAGCTGCTTACCTTGGTATGGCCTCAT  
TATATATGTTGTTCAGACCATCCTTCTACCAAATGCAGCCCCAAATCCATTGCAAACAGTC  
TTCTGGATCAGACTGTTGTTATCTGGTGTGGAGTAAGTGCACCTAGCATGCTGACTTGCTC  
ATCAGTTTGCACAGTGGCAATTGGACTGATTAGAACAGAAACTCCATTGGAACCCCGAGG  
ACAAAGGTTATGTGCTCACATGACTACTGCAGCAGAATGGTCTATGTCATTTCCTTCTT  
GGTTTTCTGACTTACATTGTTGATTTCTGAAATTTCTTACGGGTGGAAGCCAATTACA  
TGGATTAACCCCTATGACACTGCACCTTGCCTATTAAACAATGAACGAACACGGCTACTTCCA  
GAGATATTGATGAAAGGATAAAATATTCTGTAATGATTGATTCTCAGGGATTGGGAAAGG  
TTCACAGAAAGTTGCTTATTCTCTGAAATTTCACCACTTAATCAAGGCTGACAGTAACACT  
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTGATAGATTATTCTAAAGGATATCAT  
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTATCTCAGAAAATAAAGTCAAAAGACT  
ATG

## **FIGURE 2**

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV  
LCIATIYVRYKQVHALSPEENVIILKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG  
MGSLYMFVQTILSYQMOPKIHGKQVFIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW  
NPEDKGYVLHMITTAAEWSMSFSFFGFLTYIRDQKISLRVEANLHGLTLYDTAPCPINNERTR  
LLSRDI

**Important features:**

**Type II transmembrane domain:**

amino acids 13-33

**Other Transmembrane domains:**

amino acids 54-73, 94-113, 160-180, 122-141

**N-myristoylation sites.**

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

### **FIGURE 3**

CGGACCGCTGGCGGACCGTGGGGAGAGCCGCAGTCGGCTGCAGCACCTGGGAGAAGGCAGACC  
GTGTGAGGGGGCTGTGGCCCCAGCGTGTGGCTCGGGAGTGGAAAGTGGAGGCAGGAGCCTTC  
CTTACACTTCGCCTGAGTTCCTCATCGACTCCAGCATCATGATTACCTCCAGATACTATTTTG  
GATTTGGGTGGCTTCTTCATGCCAATTGTTAAAGACTATGAGATACTGTCAGTATGTTGACAG  
GTGATCTCTCCGTGACGTTGCATTTCTGCACCATGTTGAGCTCATCATCTTGAATCTTAGG  
AGTATTGAATAGCAGCTCCGTTATTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGG  
TTTCATGGTGCCTTTTACATGGCTATTTATTGTGAGCAATATCCGACTACTGCATAAACACGA  
CTGCTTTTCCTGCTCTTATGGCTGACCTTATGTATTCTCTGGAAACTAGGAGATCCCTTCC  
CATTCTCAGCCAAAACATGGATCTTACATAGAACAGCTCATCAGCCGGTTGGTGTGATTGGAG  
TGACTCTCATGGCTCTTCTGGATTGGCTGTCAACTGCCATACACTACATGTCTTACTTC  
CTCAGGAATGTGACTGACACGGATATTCTAGGCCGGACTGCTGCAAACCATGGATATGAT  
CATAAAGAAAAAGAAAAGGATGCAATGGCACGGAGAACATGTCAGAAGGGGAAGTGCATAACA  
AACCATCAGGTTCTGGGAATGATAAAAAGTGTACCACCTCAGCATCAGGAAGTGAAAATCTTACT  
CTTATTCAACAGGAAGTGGATGCTTGGAAAGAATTAAGCAGGCAGCTTTCTGGAAACAGCTGATCT  
ATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTCAAGGGAAATATTTAATTCTGGTT  
ACTTTCTCTATTACTGTGTTGGAAAATTTCATGGTACCATCAATATTGTTGATCGAGTT  
GGGAAAACGGATCCTGTACAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTGATGT  
GAAGTTTGGTCCAACACATTCTTCATTCTGTTGGAATAATCATCGTCACATCCATCAGGGAT  
TGCTGATCACTTACCAAGTTCTTATGCCATCTCTAGCAGTAAGTCCCAATGTCATTGCTCG  
CTATTAGCACAGATAATGGCATGTACTTGTCTCTGTGCTGATCGAATGAGTATGCCCTT  
AGAATACCGCACCATAACTGAAGTCCTGGAGAACTGCAGTTCAACTCTATCACCGTTGGTTG  
ATGTGATCTCCTGGTCAGCGCTCTCTAGCATACTCTTCTCTATTGGCTCACAAACAGGCACCA  
GAGAAGCAAATGGCACTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTCAAATTAA  
GATATAAGAGGGGGAAAATGAAACCAGGGCTGACATTATAAACAAACAAATGCTATGGTAGC  
ATTTTCACCTCATAGCATACTCTTCCCGTCAGGTGATACTATGACCATGAGTAGCATCAGCCAG  
AACATGAGAGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCGTGGATATGAGGCTGG  
TGTAGAGGCCAGAGGGAGGCCAAGAAACTAAAGGTGAAAATACACTGGAACCTGGGAAGACATGT  
CTATGGTAGCTGAGCCAACACGTAGGATTCCGTTAAGGTTACATGGAAAGGTTAGCTTGC  
CCTTGAGATTGACTCATTAAATCAGAGACTGTAACAAAAAAAAAAAGGGCGGCCCG  
ACTCTAGAGTCGACCTGCAGAAGCTGGCCGCATGGCCCAACTGTTATTGCAGCTTATAATG

## **FIGURE 4**

MSFLIDSSIMITSQLFFGFGWLFFMRQLFKDYEIRQYVQVIFSUTFAFSCTMFELIIFEILGV  
LNSSSRYFHWKMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTMYFFWKLGD  
FPILSPKHGILSIEQLISRVGVIGVTIMALLSGFGAVNCPTYMSYFLRNVTDTDILALERRLLQ  
TMDMIISKKRMAMARRTMFQKGEVHNKPSGFWMIKSVTTSASGSENLTLIQQEVDALEELSRQ  
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGKTDPVTRGIEI  
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLAQMIMGMY  
FVSSVLLIRMSMPLYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

**Important features:**

**Signal peptide:**

amino acids 1-23

**Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

**Eukaryotic cobalamin-binding proteins**

amino acids 151-160

## **FIGURE 5**

AGCAGGGAAATCCGATGTCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGTTCC  
AGAACTCTCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCACTGGCCATCTGAGGT  
GTTTCCCTGGCTCTGAAGGGTAGGCAGTGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT  
TCCATCTGGACCACGAGGCTCTGGCCAAGGCTTTGCGTGCAGAAGAGCTTCCATCCAGGT  
GTCATGCAGAATTATGGGATCACCCCTGTGAGCAAAGGCGAACAGCAGCTGAATTCACAG  
AAGCTAAGGAGGCCGTAGGCTGCTGGACTAAGTTGCCGGCAAGGACCAAGTTGAAACAGCC  
TTGAAAGCTAGCTTGAACCTTGCACTATGGCTGGGTTGGAGATGGATTGTCATCTCTAG  
GATTAGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTGTGATTGAAAGGTTCCAGTGA  
GCCGACAGTTGCACTTACACTCATCTGATACTTGGACTAACCTGCAATTCCAGAA  
ATTATCACCAACAAAGATCCCATTCAACACTCAAAACTGCAACACAAACAGAATTATG  
CAGTGACAGTACCTACTCGTGGCATTCCCCTACTCTACAATACCTGCCCCACTACTCTC  
CTGCTCCAGCTCCATTCTATTCACGGAGAAAAAATGATTGTCAGAGTTTATG  
GAAACTGACCATGTCTACAGAAACTGAACCAATTGTTGAAATAAAAGCAGCATCAAGAATGA  
AGCTGCTGGGTTGGAGGTGTCACCGCCTGCTAGTGCTTCTCTCTTGGTGTG  
CAGCTGGCTTGGATTTCGCTATGTCAAAAGGTATGTGAAGGCCCTCCCTTACAAACAAGAAT  
CAGCAGAAGGAAATGATGAAACCAAAGTAGTAAGGAGGAGAAGGCCAATGATAGCAACCTAA  
TGAGGAATCAAAGAAAATGATAAAAACCCAGAAGAGTCAAGAGTCAAGCAAACACTACCGTGC  
GATGCCAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTT  
CATGCTCTTACCCGCCCCAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAAGAAAGTCCA  
CCCTGGTTCTAACTGGAATCAGCTCAGGACTGCCATTGACTATGGAGTGCACCAAAGAGAAT  
GCCCTTCTCCTTATTGTAACCCGTCTGGATCCTATCCTCCTACCTCAAAGCTCCCACGCC  
TTCTAGCCTGGCTATGTCTTAATAATATCCACTGGGAGAAAGGAGTTTCAAAGTGCAGGAC  
CTAAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTCTGGCTGTGAGGCTAGGTGGTTG  
AAAGCCAAGGAGTCAGTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGACCCCTTCTCA  
GCTCTGAAAGAGAACACGTATCCCACCTGACATGCTCTCTGAGCCGGTAAGAGCAAAGAAT  
GGCAGAAAAGTTAGCCCCCTGAAGCCATGGAGATTCTATAACTTGAGACCTAATCTGTAAA  
GCTAAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGAAAC  
ACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGAATCACTGTTAGAACACACACA  
CTTACTTTCTGGCTCTACCACTGCTGATATTTCTCTAGAAATATACTTTACAAGTAACA  
AAAATAAAACTCTTATAAATTCTATTGAGTTACAGAAATGATTACTAAGGAAGATT  
ACTCAGTAATTGTTAAAAGTAATAAAATTCAACAAACATTGCTGAATAGCTACTATATGTC  
AAAGTGTGCAAGTATTACACTCTGTAATTGAATATTATCCTCAAAAATTGCACATAGTAG  
AACGCTATCTGGAGCTATTTCTCAGTTGATATTCTAGCTATCTACTTCCAAACTAAT  
TTTATTTGCTGAGACTAATCTTATTCTAATATGGCAACCATTATAACCTTAATT  
TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTAAAAGTGC  
ATTAACAAATGATCACTAGCCCTCTTTTCCAACAAGAAGGACTGAGAGATGCAGAAATT  
TGTGACAAAAAATTAAAGCATTAGAAAATT

## **FIGURE 6**

MARCFSLVLLTSIWTTTRLLVQGSLRAEELS IQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG  
LSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNSPKCGKNGVGVLIWKPVSRQFAAYCYN  
SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTPPAPASTSIPR  
RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK  
RYVKAFFPTNKNQQKEMIETKVVKEEKANDSNPNEESKTDKNPEESKSPSKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 7**

CGCCGCGCTCCCGCACCGCGGGCCGCCACCGCGCCGCTCCGCATCTGCACCCGCAGCCCCGC  
GGCCTCCCGCGGGAGCGAGCATCCAGTCCGGCCCGAGCGCAACTCGGTCCAGTCGGGGCG  
CGGCTGCGGGCGCAGAGCGGAGATGCAGCGCTTGGGGCCACCCTGCTGTGCCTGCTGCG  
CGGCGGTCCCCACGGCCCCCGGCCGCTCCGACGGCACCTCGGCTCCAGTCAAGCCGGCC  
GCTCTCAGTACCCGAGGAGGCCACCCCTAATGAGATGTTCCGAGGGTTGAGGAACGTGAT  
GGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGTA  
AAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCCAGCTATACAATGAGACCAACACAGAC  
ACGAAGGTTGAAATAATACCATCCATGTGACCGAGAAATTACAAGATAACCAACAACCAGAC  
TGGACAAATGGTCTTTCAGAGACAGTTACATCTGTGGGAGACGAAGAAGGCAGAAGGG  
ACGAGTGCATCATCGACGAGGACTGTGGGCCAGCATGTACTGCCAGTTGCCAGCTCCAGTAC  
ACCTGCCAGCCATGCCGGGCCAGGGATGCTCTGCACCCGGGACAGTGAGTGTGGAGACCA  
GCTGTGTCTGGGTCACTGCACCAAAATGCCACCAAGGGGAGCAATGGGACCATCTGTGACA  
ACCAAGAGGGACTGCCAGCCGGGCTGTGCTGTGCCATTCCAGAGAGGCCAGCTGTCCCTGTG  
ACACCCCTGCCGTGGAGGGCGAGCTTGCATGACCCCGCCAGCCGGCTCTGGACCTCATCAC  
CTGGGAGCTAGAGCTGTGGAGCCTTGGACCGATGCCCTGTGCCAGTGGCCTCCTCTGCCAGC  
CCCACAGCCACAGCCTGGTGTATGTGCAAGCCGACCTCGTGGGAGCCGTGACCAAGATGG  
GAGATCCTGCTGCCAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTTCATGGAGGAGGTGCG  
CCAGGAGCTGGAGGACCTGGAGGGAGCCTGACTGAAGAGATGCCGTGGGGAGCCTGCCAGT  
CCGCCGCTGCACTGCTGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGTAGATGTGCAA  
TAGAAATAGCTAATTATTCAGGTGTGCTTAGCGTGGGTGACCAAGGCTTCTCCTA  
CATCTCTCCAGTAAGTTCCCCTGGCTGACAGCATGAGGTGTTGCAATTGTCAGCT  
CCCCCAGGCTTCTCCAGGCTTCACAGTCTGGTGTGGAGAGTCAGGCAGGGTTAAACTGCA  
GGAGCAGTTGCCACCCCTGTCCAGATTATGGCTGCTTGCCCTACAGTTGCCAGACAGCG  
TTTGTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAATGTGGAGTCTCCCT  
TGATTGGTTTGGGAAATGTGAGAAGAGTGCCTGCTTGCAACATCAACCTGGAAAAATG  
CAACAAATGAATTTCACGCAGTTCTTCATGGCATAGGTAAGCTGTGCCCTCAGCTGTG  
AGATGAAATGTTCTGTCACCTGCAATTACATGTGTTATTCACTCCAGCAGTGTGCTCAGCTCC  
TACCTCTGTGCCAGGGAGCATTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGG  
AGGGGTCAATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTGCC  
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCATCTGGTGTGACTCTAACGCTCAGTGTCT  
CTCCCACTACCCACACCCAGCCTGGTGCACCAAAAGTGTCCCCAAAAGGAAGGAGAATGGGAT  
TTTCTTGAGGCATGCACATGTGAATTAAAGTCACAAACTAATTCTCACATCCCTCTAAAGTAAA  
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCGTCCTCTAATGAAGACAATGAT  
ATTGACACTGTCCCTTTGGCAGTTGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCA  
TACAGGTTAACCTGCAAAACAGTACTTAGTAATTGAGGGCGAGGATTATAATGAAATTG  
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGC  
TGTGTGAAACATGGTTGAATATGCACTGCGAACACTGAACCTACGCCACTCCACAAATGATG  
TTTCAGGTGTATGGACTGTTGCCACCATGTATTCACTCCAGGTTCTAAAGTTAAAGTTGCA  
CATGATTGATAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTGCATTAGAA  
ATCAAGCATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

## **FIGURE 8**

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL  
RSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDKVGNNTIHVHREIHKITNNQTGQMVFSE  
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCGDQLCVWGHC  
TKMATRGNSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRLLDLITWELEPDG  
ALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQELEDLE  
RSLTEEMALGEPAAAAALLGGEEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 9**

CGGACGCGTGGCGGACGCGTGGGGCTGTGAGAAAGTCCAATAAATACATCATGCAACCCAC  
GGCCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCAGGGCTACTCATCCAAAG  
GCCTAATCCAACGTTCTGTCTCAATCTGCAAATCTATGGGTCTGGGCTTTCTGGACCTT  
AACTGGGTACTGGCCTGGCCAATGCGTCTCGTGGAGCCTTGCCCTTACTGGCCTT  
CCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTGCTTCATCCGACACTCCGTTACC  
ACACTGGGTCAATTGGCATTGGAGCCCTACCTGACCCCTGTGCAAGATAGCCCCGGTCATCTTG  
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCTGTAGCCCGCTGCATCATGTGCTGTTT  
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTATCAAGTCTAAACCGCAATGCATACATCATGA  
TCGCCATCTACGGGAAGAATTCTGTCTCAGCCAAAATGCGTTCATGCTACTCATGCGAAC  
ATTGTCAGGGTGGTCGTCTGGACAAAGTCACAGACCTGCTGCTTCTGGGAAGGCTGCTGGT  
GGTCGGAGGCGTGGGGCTCTGCTCTTTCTCCGGTCGCATCCGGGCTGGTAAAG  
ACTTTAAGAGCCCCCACCTCAACTATTACTGGCTGCCCATGACCTCCATCCTGGGGCCTAT  
GTCATGCCAGCGGCTTCTCAGCTTCCGGCATGTGTGACACGCTTCCCTGCTTCCT  
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTCTAA  
AGATTCTGGGCAAGAAGAACGAGGCGCCCCCGACAACAAGAAGAGGAAGAAGTGACAGCTCCG  
CCCTGATCCAGGACTGCACCCACCCCAACCGTCCAGCCATCCAACCTCACTTCCCTACAGGT  
CTCCATTGTGGTAAAAAAAGTTTAGGCCAGGCGCCGTGGCTCACGCTGTAATCCAACACT  
TTGAGAGGCTGAGGCCGGGATCACCTGAGTCAGGAGTTCGAGACCAAGCCTGGCAACATGGTG  
AAACCTCCGTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCACTCCA  
GCTACTCGGAGGCTGAGGCAGGAGAATCGCTGAACCCGGAGGCAGAGGTTGCAGTGAGCCGA  
GATCGGCCACTGCACCTGGGTGACAGACTCTGTCTCCAAAACAAACAAACAAA  
AAGATTTTATTAAAGATATTGTAACTC

## **FIGURE 10**

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVGLFWTL  
NWVLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL  
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN  
IVRVVVLDKVTDLLLFFGKLLVVGVGVLSSSSSGRIPLGKDFKSPHLNYYWLPIMTSILGAY  
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYMSKSLLKILGKKNEAPPDNKKRKK

**Important features:**

**Transmembrane domains:**

amino acids 57-80 (type II), 110-126, 215-231, 254-274

**N-glycosylation sites.**

amino acids 16-20, 27-31, 289-293

**Hypothetical YBR002c family proteins.**

amino acids 276-288

**Ammonium transporters proteins.**

amino acids 204-231

**N-myristoylation sites.**

amino acids 60-66, 78-84

**Amidation site.**

amino acids 306-310

### **FIGURE 11**

GCCCCCGCCGCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCTGGGGCCTGCCTGGGAGCCCTGC  
TCCCTGCTCAGCTGCCGTCTGCCCTGCGGCTCTGCCCTGCATCTGTGCAGCTGCTGCCCGC  
CAGCCGCAACTCCACCGTGAGCCGCTCATCTCACGTTCTCCTCTTCTGGGGTGCTGGTGTCCA  
TCATTATGCTGAGCCGGCGTGGAGAGTCAGCTTACAAGCTGCCCTGGGTGTGAGGAGGGGCC  
GGGATCCCCACCGTCTGCAGGGCACATCGACTGTGGCTCCCTGCTGGCTACCGCCTGTCTACCG  
CATGTGCTTCGCCACGGCGGCCCTCTTCTTCTTCTACCCCTGCTCATGCTCGCGTGAGCAGCA  
GCCGGGACCCCCGGCTGCCATCCAGAATGGGTTGGTTCTTAAGTCCGTATCCTGGTGGCCTC  
ACCGTGGGTGCCCTCTACATCCCTGACGGCTCTCACCAACATCTGGTCTACTTCGGCGTGTGG  
CTCCTCTCTCATCCTCATCCAGCTGGTGTGCTCATCGACTTGCACACTCCTGGAACCGAGGGT  
GGCTGGGAAGGCCGAGGAGTGCATTCCCGTGCCTGGTACGCAGGCCCTTCTTCACTCTCCTC  
TTCTACTTGCTGTCGATCGCGCCGTGGCGCTGATGTTCATGTACTACTACACTGAGGCCAGCGGCTGCCA  
CGAGGGCAAGGTCTCATCAGCCTAACCTCACCTCTGTGTCTGCCTGCCATCGCTGTCTGC  
CCAAGGTCCAGGACGCCAGCCAACTCGGGCTGCTGCAGGCCCTGGTCATACCCTACACCAGT  
TTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTGCCAACCCAGCT  
GGGCAACGAGACAGTTGTGGCAGGCCAGGGCTATGAGACCCAGTGTGGGATGCCAGGCCATTG  
TGGGCCTCATCATCTCCCTGTGCACCCCTTCTCATCAGTCTGCCTCCTCAGACCACCGGCAGGTG  
AACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAG  
GGCAGCCTGTGAGGGCGGGCTTGACAACCGAGCAGGCCAGGGCTCACCTACAGTACTCCTCTCC  
ACTTCTGCCCTGGTGTGGCTGCCACTGCACGTATGATGACGCTACCAACTGGTACAAGCCGGTGA  
ACCCGGAAAGATGATCAGCACGTGGACGCCGTGGGTGAAGATCTGTGCCAGCTGGCAGGGCTGC  
CCTCTACCTGTGGACCCCTGGTAGGCCACTCCTGCCACCGCAGCTGGCAGGCCCTCA  
CAGCCTGCCATCTGGTGCCTCTGCCACCTGGTGCCTCTGGCTCGGTGACAGCCACCTGCCCTC  
CCCACACCAATGCCAGGCTGAGCCCCACCCCTGCCAGCTCCAGGACCTGCCCTGAGCCGGG  
CTTCTAGTCGTAGTGCCTCAGGGTCCGAGGAGCATCAGGCTCTGCAGAGCCCCATCCCCCGCCAC  
ACCCACACGGTGGAGCTGCCCTTCCCTCCCTGTTGCCATAACTCAGCATCTGGATGAA  
AGGGCTCCCTGTCTCAGGCTCCAGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACTCCACACAG  
TGGGGCATCCGGCACTGAAGCCCTGGTGTCCCTGGTACGTCCCCCAGGGACCCGTCCCCCTTCTG  
GACTTCGTGCCTTACTGAGTCTAAGACTTTCTAAAACAAGCCAGTGCCTGAAAAAAA

## **FIGURE 12**

MGACLGACSLLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVESQL  
YKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFTLLMLCVSSSRDPRAAIQ  
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQVLVLLIDFAHAWNQRWLGKAE  
ECDSRAWYAGLFFFITLLFYLLSIAAVALMFYYTEPSGCHEGKVFISLNLTFCVCVSIAAVLPKV  
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPS  
VGLIIIFILLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVAACEGRAFDNEQDGVTYSY  
SFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICASWAGLLLWTLVAPLLLNRD  
FS

**Signal sequence:**

amino acids 1-20

**Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

### **FIGURE 13**

CGGGCCAGCCTGGGGCGGCCGCCCCAGGAACCACCCGTTAAGGTGTCTTCTCTTAGGGATGGTGA  
GGTTGAAAAAGACTCCTGTAACCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAGAACG  
CTCTCACCGGGAGCCAGAGCTCCCATGCTTCCTGCGCAATATCCATTCCATCAACCCCCACACAA  
CTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC  
TTTCTGTTGTTGTCACCTTGACCTCTTATTGTAACATTACTGTGGATAATAGAGTTAAATG  
TGAATGGAGGCATTGAGAACACATTAGAGAAGGGAGGTGATGCAGTATGACTACTATTCTCATAT  
TTTGATATATTTCTCTGGCAGTTTCGATTTAAAGTGTAAACTTGCATATGCTGTGTCAG  
ACTGCGCCATTGGTGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTACTAGCAAAG  
TGATCCTTCGAAGCTTCTCAAGGGGCTTGGCTATGTGCTGCCATCATTCATTCACTC  
CTTGCCTGGATTGAGACGTTCTGGATTCAAAGTGTACCTCAAGAAGCAGAAGAAGAAAA  
CAGACTCCTGATAGTTCAAGGATGCTTCAGAGAGGGCAGCACTTACCTGGTGGCTTCTGATG  
GTCAGTTTATTCCCCCTCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT  
GAGAAACCACTTAGAACTATGAGTACTACTTTGTTAAATGTGAAAAACCTCACAGAAAGTC  
ATCGAGGCAAAAGAGGCAGGCAGTGAGTCTCCCTGTCGACAGTAAAGTGAATGGTACGTC  
CACTGCTGGCTTATTGAACAGCTAATAAGATTATTGTAAACCTCACAAACGTTGAC  
CATATCCATGCACATTAGTGCCTGCCTGAGCTGGTAAGGTAAATGTCATGATTCACTCTCT  
TCAGTGAGACTGAGCCTGATGTGTTACAAATAGGTGAAGAAAGTCTTGCTGTATTCTAATC  
AAAAGACTTAATATATTGAAGTAACACTTTTAGTAAGCAAGATAACCTTTTATTCAATTCA  
AGAATGGAATTTTGTTCATGTCAGATTATTTGTATTCTTTAACACTCTACATT  
TCCCTGTTTTAACTCATGCACATGTGCTTTGTCAGTTAAAAGTGTAAATAAATCTG  
ACATGTCAATGTTGCTAGTTTATTCTGTTGCATTATGTGTATGGCCTGAAGTGTGGA  
CTTGCAAAAGGGAAAGAAAGGAATTGCGAATACATGTAATGTCACCAGACATTGTATTATT  
TTATCATGAAATCATGTTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTGAAATGC  
ACAAAATGACTAAACCATTCATGTTCTTGCCTGCGTCAGCCAATTCAATTAAAATGAA  
CTAAATTAAAAA

## **FIGURE 14**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF  
VTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT  
AVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPOEAEEENRLLIVQDASER  
AALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

**N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

## **FIGURE 15**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTGGGCCGACCCGCCAGGAAAGACTGAGG  
CCGC GG CCT GCCC CG CC GG CT CC TG CG CC GG CC GG CT CC CG GG AC AGA AG AT GT G CT CC AG  
GGT CCC CT TG CT TG CT GG CG CT GT CT CT G T ACT GG CC CT GG GG CT GG GG TG CA GG G CT G CC CAT  
CCGG CT GC CAG TG CAG CC AG CC AC AG AC AG T CT TG C ACT G C CC GG CC AG GG G ACC AC GG TG CC  
CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTGAGAACGGCATCACCATGCTGACGC  
AGGCAGCTTGCGGCCTGCCGGGCTGCAGCTCCTGGACCTGTACAGAACAGATGCCAGCC  
TGCCCAGCGGGGTCTTCCAGCCACTGCCAACCTCAGCAACCTGGACCTGACGCCAACAGGCTG  
CATGAAATACCAATGAGACCTCCGTGGCTGCGGCCCTCGAGGCCCTACTGGCAAGAA  
CCGCATCCGCCACATCCAGCCTGGTGCCCTCGACAGCCTGACCCTCTGGAGCTCAAGCTGC  
AGGACAACAGAGCTGCCGGCACTGCCCGCTGCCGCTGCCCGCCCTGCTGCTGGACCTCAGC  
CACAACAGCCTCTGGCCCTGGAGGCCGATCCTGGACACTGCCAACCTGGAGGCGCTGCCG  
GGCTGGTCTGGGCTGCAAGCTGGACGGGGCTCTCAGCCGCTTGCGCAACCTCCACGACC  
TGGATGTGTCCGACAACCAGCTGGAGCGAGTGGCACCTGTATCCGAGGCCCTGGAGCTGACG  
CGCCCTGCCGGCTGGCCGGCAACACCCGCAATTGCCAGCTGCCGGGGAGGACCTGCCGGGCTGGC  
TGCCCTGCAAGCTGGATGTGAGCAACCTAAGCTGCAAGGCCCTGGCTGGCGACCTCTGGGCC  
TCTTCCCCCGCCTGCGCTGCTGGCAGCTGCCGCCAACCCCTTCACACTGCGTGTGCCCCCTGAGC  
TGGTTTGGCCCTGGGTGCGCAGAGCCACGTACACTGGCAGGCCCTGAGGAGACGCCGCTGCCA  
CTTCCCCCCAAGAACGCTGCCGGCTGCTCTGGAGCTTGACTACGCCACTTTGGCTCCCCAG  
CCACCACCACACAGCCACAGTGCCAACACAGCAGGCCGAGGCCACTGAGGCCACGCCCTGTCT  
TCTAGCTTGGCTCTTACCTGGCTTAGCCCCACAGCAGGCCACTGAGGCCACCGTCCACCTGCCCTCA  
CACTGCCAACCGACTGTAGGGCTGTCCCCAGGCCAGGACTGCCCACCGTCCACCTGCCCTCA  
ATGGGGCACATGCCACCTGGGACACGGCACCCACTGGCGTGTGCTTGCCCCGAAGGCTTACG  
GGCCTGACTGTGAGAGCCAGATGGGGCAGGGGACACGCCAGGCCCTACACCAGTCAGCCGAG  
GCCACCACGGTCCCTGACCCCTGGCATCGAGCCGGTGAAGCCCCACCTCCCTGCCGTGGGCTGC  
AGCGTACCTCCAGGGAGCTCCGTGCAAGCTCAGGAGCCTCCGTCAACCTATCGAACCTATCG  
GGCCCTGATAAGCGCTGGTGACGCTGCGACTGCCCTGCCCTCGCTCGTGAAGTACACGGTACCCA  
GCTGCCGCCAACGCCACTTACTCCGTCTGTGTCATGCCCTGGGGCCGGGGCTGGGGAGG  
GCGAGGAGGCCTGGGGAGGCCATACACCCCAAGCCGCTCCACTCCAACACGCCAGTCACC  
CAGGCCCGAGGGCAACCTGCCCTCCTCATGGCCCGCCCTGGCGGGTGTCCCTGGCCG  
GCTGGCTGCCGTGGGGCAGCTACTGTGTGCGGCCGGGCCATGGCAGCAGCGCTCAGG  
ACAAAGGGCAGGTGGGCCAGGGCTGGCCCTGGAACCTGGAGGGAGTGAAGGCTCCCTGGAG  
CCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTGTGAGTGTGAGGTGCC  
ACTCATGGCTTCCCAGGGCTGCCCTCCAGTCACCCCTCCACGCAAAGCCCTACATCTAAGCCA  
GAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGATGCCAGGCCCTCTGCTGCC  
ACACCAACGTAAGTCTCAGTCCAACCTGGGATGTGTCAGACAGGGCTGTGACCAAGCT  
GGGCCCTGTTCCCTGCGACCTGGCTCGGTCTCCATCTGTGAGATGCTGGCCAGCTGACGAGCC  
CTAACGTCCTCCAGAACCGAGTGCTCATGAGGACAGTGCTCCGCTGCCCTCCGCAACGTGCA  
CCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCACTGCCCTGGGTCTGCTGGCTCTCCAC  
TCCAGGGCGGCCCTGGGGCCAGTGAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGC  
GGCTGTGTGACTCTAGTCTTGGCCCGAGGAAGCGAAGGAACAAAAGAAAAGTGGAAAGGAAGATGC  
TTTAGGAACATGTTTGTCTTTAAAATATATATTATAAGAGATCCTTCCCATTATCT  
GGGAAGATGTTTCAAACTCAGAGACAAGGACTTGGTTTGTAAGACAAACGATGATATGAA  
GGCTTTGTAAGAAAAATAAAAGATGAAGTGTGAAA

## **FIGURE 16**

MCSRVPILLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQTTVPRDVPPDTVGLYVFENGIT  
MLDAGSFAGLPGLQLLDSQNQIASLPSGVQPLANLSNLDLTANRLHEITNETFRGLRRLERLY  
LGKNRIRHIQPGAFDTLDRLLELKLDNELRALPPLRLPRLLLLDLSHNSLLALEPGILDGTANVE  
ALRLAGLGLQQLDEGLFSRLRNLDLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDL  
AGLAALQELDVSNLSQLPGDLSGLFPRLLAARNPFCNCVCPLSWFGPWVRESHVTLASPEE  
TRCHFPPKNAGRLLLEDYADFGCPATTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAP  
SPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTP  
VTPRPPRSLTGLIEPVSPSTSRLVGLQRYLQGSSVQLRSRLTYRNLSGPDKRLVTLRLPASLA  
TGTQLRPNATYSVCVMPLGPGRVPEGEAACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAA  
LLAALAAVGAAAYCVRGRAMAQAQDKGQVPGPAGPLELEGVKVPLEPGPKATEGGEALPSGSE  
CEVPLIMGFPGPGLQSPLHAKPYI

**Important features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 579-599

**EGF-like domain cysteine pattern signature.**

amino acids 430-442

**Leucine zipper pattern.**

amino acids 197-219, 269-291

**N-glycosylation sites.**

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

**Tyrosine kinase phosphorylation sites.**

amino acids 124-131, 337-345

**N-myristoylation sites.**

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,  
594-600, 640-646

## **FIGURE 17**

GCAGCGCGAGGC GGCGGTGGTGGCTGAGTCCTGGTGGCAGAGGCAGAGCTCATGCG  
GGTCCGGATAGGGCTGACGCTGCTGCTGTGCGGTGCTGAGCTTGGCTCGCGTCCTCGG  
ATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTGACATCAGATGAGTCAGTA  
AAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTCTTGATTCAAAGAAATCTGA  
ATTAGAACCTCTATTCAAGAACAGGAGAACAGCCTCAAGAGCCAAGAGGGGGAAAGTGTACAG  
AAGATATCAGCTTCTAGAGTCAGAACTCAGAAAACAAGGACTATGAAGAGCCAAGAAAGTA  
CGGAAACCAGCTTGACGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTCCCTTTCT  
TTTCCTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAAGATGGCAGACTGTGGTGTG  
CTACAAACCTATGACTACAAAGCAGATGAAAAGTGGGCTTTGTGAAACTGAAGAACAGGCTGCT  
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTACACTGAAATGAAAATCCTTAATGAAAG  
CAATAAGAAAAGCCAAAAAGAGAACATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA  
CCAAAGCCCTGGAGAGAGTGTCAATGCTCTTTATTGGTGAATTACTGCCACAGAATATCCAG  
GCAGCGAGAGAGATTTGAGAAGCTGACTGAGGAAGGCCTCCCAAGGGACAGACTGCTTTGG  
CTTTCTGTATGCCTCTGGACTTGGTGTAAATTCAAGTCAGGCAAAGGCTCTGTATATTACAT  
TTGGAGCTCTGGGGCAATCTAATAGCCCACATGGTTTGTAAAGTAGACTTTAGTGGAAAGGCT  
AATAATATTAACATCAGAAGAATTGTGGTTATAGCGGCCACAACCTTTCAGCTTCATGATC  
CAGATTGCTGTATTAAGACCAAATTCAGTTGAACCTCCTCAAATTCTGTAAATGGATAT  
AACACATGGAATCTACATGTAATGAAAGTGGTGGAGTCCACAATTTCCTTAAATTTCTGTAGTTG  
TTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGCTCTTTAAATTTCTGTAGTTCA  
AAATTTGTAAATGGTGGTATAGAAAACACATGAAATATTATACAAATTTGCAACAATGC  
CCTAAGAATTGTTAAATTCTGGAGTTATTGTGCAAGACTCCAGAGAGCTCTACTTCG  
TTTTTACTTTCATGATTGGCTGTCTCCATTCTGGTCAATTATTGCTAGTGACACTGT  
GCCTGCTTCCAGTAGTCTCATTTCCATTGGCTAATTGTTACTTTCTTGCTAATTGG  
AAGATTAACTCATTTAATAAAATTATGCTAAGATTAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 18**

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLSKTTLTSDESVKDHTAGRVVAGQIFLDSEEESEL  
ESSIQEEEDSLKSQEGERVTEDISFLESPNPNENKDYEPPKKVRKPALTAIEGTAHGEPCHPFLFLDK  
EYDECTS DGDREDGRLWCATTYDYKADEKWGFCETEEEAKRRQMQEAEMMYQTGMKILNGSNKKSQKR  
EAYRYLQKAASMNHTKALERVSYALLFGDYLQPQNIQAAREMFEKLTEEGSPKGQTALGFLYASGLGVN  
SSQAKALVYYTFGALGGNLIAHMVLVSRL

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 195-199, 217-221, 272-276

**Tyrosine kinase phosphorylation site.**

amino acids 220-228

**N-myristoylation sites.**

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

**Glycosaminoglycan attachment site.**

amino acids 267-271

**Microbodies C-terminal targeting signal.**

amino acids 299-303

**Type II fibronectin collagen-binding domain protein.**

amino acids 127-169

**Fructose-bisphosphate aldolase class-II protein.**

amino acids 101-119

## **FIGURE 19**

AATTCAAGATTTAAGCCCATTCTGCAGTGGAAATTCACTGAACTAGCAAGAGGACACCATCTTCTT  
GTATTATAACAAGAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTGGGTGCTAGG  
CCTCCTAACCTCTGTGGTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAGACATCACTG  
ATAAGTACATTTTATCACTGGATGTGACTCGGCTTGGAAACTTGGCAGCCAGAAACTTTGAT  
AAAAAGGGATTCATGTAATCGCTGCCTGTGACTGAATCAGGATCAACAGCTTAAAGGAGA  
AACCTCAGAGAGACTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG  
CCCAGTGGGTGAAGAACCAAGTGGGGAGAAAGGTCTCTGGGTCTGATCAATAATGCTGGTGT  
CCCAGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA  
CCTGTTGGACTCATCAGTGTGACACTAAATGCTTCCTTGGCAAGAAAGCTCAAGGGAGAG  
TTATTAAATGTCTCCAGTGTGAGGTCGCCTGCAATCGTGGAGGGGGCTATACTCCATCCAAA  
TATGCAGTGGAAAGGTTCAATGACAGCTTAAGACGGGACATGAAAGCTTGGGTGCACGTCTC  
ATGCATTGAACCAGGATTGTTCAAAAACAAACTGGCAGATCCAGTAAAGGTTAATTGAAAAAAAC  
TCGCCATTGGAGCAGCTGTCTCCAGACATCAAACAACAAATATGGAGAAGGTACATTGAAAAAA  
AGTCTAGACAAACTGAAAGGCAATAACCTATGTGAACATGGACCTCTCCGGTGGTAGAGTG  
CATGGACCACGCTCAACAAAGTCTCTCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAA  
TTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTGCAAGACTTTTATTGTTGAAACAGAAA  
GCAGAGCTGGCTAACCCCAAGGCAGTGTGACTCAGCTAACACACAAATGTCTCCCCAGGCTATGA  
AATTGGCCGATTCAAGAACACATCTCCTTCAACCCATTCCTTATCTGCTCAACCTGGACT  
CATTTAGATCGTGCTTATTGGATTGCAAAGGGAGTCCCACCATCGCTGGTGGTATCCAGGG  
CCCTGCTCAAGTTTCTTGAAAGGAGGGCTGGATGGTACATCACATAGGCAAGTCCTCGCCT  
GTATTTAGGCTTGCCTGCTTGGTGTGATGTTAAGGAAATTGAAAGGACTTGCCCATTCAAAATG  
TCTTACCGTGGCTGCCCCATGCTTGGTCCAGCATTTACAGTAACTTGGAATGTTAAGT  
ATCATCTCTTATCAAATTAAAAGATAAGTCAACCCAAAAAAAAAAAAAA  
AAAAAAAAAAAA

## **FIGURE 20**

MLFWVLGLLILCGFLWTRKGKLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG  
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDWLTLEDY  
REPIEVNLFGGLISVTLNMLPLVKKAQGRVINSSVGGRLAIVGGGYTPSKYAVEGFNDSLRRDMK  
AFGVHVSCIEPGLFKTNLADPVKVIKEKKLAIWEQLSPDIKQQYGEFYIEKSLDKLGNKSYVNMD  
LSPVVECMDHALTSIFPKTHYAAAGKDAKIFWIPLSHMPAALQDFLLLKQKAELANPKAV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

## **FIGURE 21**

CTGAGGC GGCGGTAGCATGGAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTGCTCGGC  
CACTCGTTCCAGCACCTAACACCGACTCGGACACGGAAGGTTCTTCTGGGAAGTAAA  
GGTGAAGCCAAGAACAGCATTACTGATTCCAAATGGATGATGTTGAAGTTGTTATAACATTGA  
CATTCAGAAATATATTCCATGCTATCAGTTTAGCTTTATAATTCTTCAGGCGAAGTAAATG  
AGCAAGCACTGAAGAAAATATTCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATTCCGT  
CGTCATTCA GATCAGATCATGACGTTAGAGAGAGGCTGCTTCACAAAAC TTGCAGGAGCATT  
TTCAAACCAAGACCTGTTCTGCTATTAAACACCAAGTATAACA GAAAGCTGCTACTC  
ATCGACTGGAACATTCCCTATATAAA CCTCAAAAAGGACTTTTCACAGGGTACCTTAGTGGTT  
GCCAATCTGGGATGTCTGAACA ACTGGTTATAAAACTGTATCAGGTTCTGTATGTCCACTGG  
TTTAGCCGAGCAGTACAAACACAGCTCTAAATTTTGAAGAAGATGGATCCTAAAGGAGG  
TACATAAGATAAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAGTG  
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAACAGATTAAAACGAGAAATTGA  
GAAAAGGAGAGGAGCACAGATT CAGG CAGCAAGAGAGAAGAACATCCAAAAGACCCTCAGGAGA  
ACATTTTCTTGTCAGGCATTACGGACCTTTTCCAAATTCTGAATTCTCATT CATGTGTT  
ATGTCTTAAAAAAATAGACATGTTCTAAAAGTAGCTGTA ACTACAACCACATCTGATGTAGT  
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCAC  
AAATCATTAAGCATAAAAGCCTAGACTTAGATGACAGATGGCAATTCAAGAGATCTGGTTGTTA  
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAACGATCCAAAAT  
GAGCAGCCCAGAAACAGATGAAGAAAAGATGAAGGGTTGGTGAATATTACCGGTCTC  
CTACATTTGATCTTTAACCTTACAAGGAGATTTTTATTGGCTGATGGTAAAGCCAAAC  
ATTC TATTGTTTACTATGTTGAGCTACTGCAGTAAGTCATTGTTTACTATGTTCA  
TGTTGCAGTAATACACAGATACTCTTAGTGCATTACTCACAAAGTACTTTCAAACATCA  
GATGCTTTATTCCAAACCTTTTACCTTCACTAAGTTGTTGAGGGAAAGGCTTACACAG  
ACACATTCTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT  
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGCAACGTATT  
GAGACCATGTCTATTAAAAAATGGAAAAGCAAGAA TAGCCTATTTCAAAATATGGAAA  
GAAATTATATGAAAATTATCTGAGTCATTAAAATTCTCCTTAAGTGATACTTTTAGAAGTA  
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAATTGCAAAACATCATCT  
AAAATTAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 22**

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLGEVKGEAKNSITDSQMDDVEVVYTIDIQKYI  
PCYQLFSFYNSSGEVNEQALKKILSNVKNNVGWYKFRRHSDQIMTFRERLLHKNLQEHSNQDL  
VFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV  
QTHSSKKFEEDGSILKEVHKINEMYASLQEELKSICKVEDSEQAVDKLVKDVNRLKREIEKRRGA  
QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHSVSKSSCNYNHHLDVVDNLTL  
MVEHTDIPEASPARTPQIIKHKALDDLDRWQFKRSRLLDTQDKRSKANTGSSNQDKASKMSSPET  
DEEIEKMKGFGEYSRSPTF

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation sites.**

amino acids 75-79, 322-326

**N-myristoylation site.**

amino acids 184-154

**Growth factor and cytokines receptors family.**

amino acids 134-150

## FIGURE 23

## **FIGURE 24**

MARFGLPALLCTLAVLSAALLAAELKSKCSEVRRLYVSKGFKNDAPLHEINGDHLKICPQGST  
CCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSNDMFVKTYGH  
LYMQNSELFKDLFVELKRYYVGPNLNEEMLNDFWARLLERMFRVLVNSQYHFTDEYLECVSKYTE  
QLKPFGDVPRKLQLQVTRAFVAARTFAQGLAVAGDVVSKVSVNPTAQCTHALLKMIYCSHCRLG  
VTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN  
MQDNSVQVSQKVFQGCGPPKPLPAGRISRSISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK  
EKLKQAKKFWSLPSNVNCNDERMAAGNGNEDDCWNGKGKSRYLFATGNGLANQGNPENVQDTS  
KPDILILRQIMALRVMTSKMKNAYNGNDVFFFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG  
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

**Important features:**

**Signal peptide:**

amino acids 1-22

**ATP/GTP-binding site motif A (P-loop).**

amino acids 515-524

**N-glycosylation site.**

amino acids 514-518

**Glycosaminoglycan attachment sites.**

amino acids 494-498, 498-502

**N-myristoylation sites.**

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

**Glypicans proteins.**

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

## **FIGURE 25**

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC  
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTCCATTATATTCTTCAGCAACT  
TACAGCTGCACCGACAGTTGCGGATGAAAGTTCTAATCTCTCCCTCCTGTTGCTGCCACTAA  
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCCAGAGGCCACAGGGACCGAGGC  
CAGGCTCTAGGAGATGGCTCCAGGAAGGCGCCAAGAATGTGAGTGCAAAGATTGGTTCCGTGAG  
AGCCCCGAGAAGAAAATTCACTGACAGTGTCTGGGCTGCCAAAGAACAGTGCCTGATCATT  
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACACAGAAAGCCAACAAGCATTCCAGA  
GCCTGCCAGCAATTCTCAAACAAATGTCAGCTAAGAAGCTTGCTCTGCCCTTGTAGGAGCTCTG  
AGCGCCCACCTTCCAATTAAACATTCTCAGCCAAGAACAGTGAGCACACCTACCAGACACTC  
TTCTTCTCCCACCTCACTCTCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAGCA  
TGTTTTCAAGATCATTGTTGCTCTCTAGTGTCTCTCGTCAGTCTTAGCCT  
GTGCCCTCCCCTAACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCC  
AGCTAGTGTCAATTAAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAACGTCAATAAATATTTT  
AAATGTCAAAAAAAAAAAAAAA

## **FIGURE 26**

MKVLISSLLLLPIMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM  
TVSGLPKKKQCPKCDHFKGKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 27-33, 46-52

## **FIGURE 27**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTCCCCAGCGGAAGCACAGCTCAG  
AGCTGGTCTGCCATGGACATCCTGGTCCCACCTCTGCAGCTGCTGGTGTGCTTCTTACCCCTGCC  
CCTGCACCTCATGGCTCTGCTGGCTGCTGGCAGCCCTGTGCAAAGCTACTTCCCTACCTGA  
TGGCCGTGCTGACTCCCAAGAGCAACCGAAGATGGAGAGCAAGAAACGGGAGCTTCAGCCAG  
ATAAAGGGCTTACAGGAGCCTCGGGAAAGTGGCCCTACTGGAGCTGGCTGCGGAACCGGAGC  
CAACTTCCAGTTCTACCCACCGGGCTGCAGGTCACTGCCTAGACCCAAATCCCACTTGAGA  
AGTTCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTGTGGCTCCT  
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGTG  
CTCTGTGCAGAGCCAAGGAAGGTCTGCAGGAGGTCCGGAGAGTACTGAGACCCGGAGGTGTG  
TCTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTC  
GAGCCCACCTGAAACACATTGGGATGGCTGCTGCCTCACAGAGAGACCTGGAAGGATCTGA  
GAACGCCAGTTCTCGAAATCCAATGGAACGACAGCCCCCTCCCTGAAGTGGCTACCTGTTG  
GGCCCCACATCATGGAAAGGCTGTCAAACAATCTTCCAAGCTCCAAGGCACTCATTGCTCC  
TTCCCCAGCCTCAATTAGAACAGCCACCCACCAGCCTATCTATCTTCACTGAGAGGGACTA  
GCAGAAATGAGAGAACATTCATGTACCACTACTAGTCCCTCTCCCAACCTTGCCAGGG  
AATCTCTAACTCAATCCGCCTCGACAGTGAAAAGCTTACTTCTACGCTGACCCAGGGAGG  
AAACACTAGGACCCGTGTATCCTCAACTGCAAGTTCTGGACTAGTCTCCAACGTTGCCTC  
CCAATGTTGTCCCTTCCCTCGTCCATGGTAAAGCTCTCGCTTCCCTGGCTACAC  
CCATGCCCTCTAGGAACTGGTCAAAAAGCTGGTGCCTGCATCCCTGCCAAGGCCCTGAC  
CCTCTCTCCCACTACCACCTTTCCCTGAGCTGGGGACCCAGGGAGAATCAGAGATGCTGGG  
ATGCCAGAGCAAGACTCAAAGAGGCAGGGTTTGTTCTCAAATTTTTTAAAATAGACGAA  
ACCACG

## **FIGURE 28**

MDILVPLLQLLVLLTLPLHIMALLGCWQPLCKSYFPYIMAVLTPKSNRKMESKKRELFSQIKGL  
TGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM  
RQLADGSMDVVVCTLVLCSVQSPRKVLQEVRVRLPFGVLFFWEHVAEPYGSWAFMWQQVFEPTW  
KHIGDGCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFPSSKALICSFPSL  
QLEQATHQPIYLPLRGT

**Important features:**

**Signal peptide:**

amino acids 1-23

**Leucine zipper pattern.**

amino acids 10-32

**N-myristoylation sites.**

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

## **FIGURE 29**

CAATGTTGCCTATCCACCTCCCCAAGCCCTTACCTATGCTGCTGCTAACGCTGCTGCTGCT  
GCTGCTGCTGCTAAAGGCTCATGCTGGAGTGGGACTGGTCGGGCCAGAAAGTCTCTCTG  
CCACTGACGCCCATCAGGGATTGGGCCTCTTCCCCCTTCCTTCTGTGTCTCCTGCCTCAT  
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGTGGGGATGGCTA  
AAGAAAGCTGGGAGATAGGGAACAGAACAGAGGGTAGTGGGTGGCTAGGGGGCTGCCTTATTTAAA  
GTGGTTGTTTATGTTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTCATTAAGAAATT  
GTTCCCTCCCTGTGTTCAATGTTGTAAGATTGTTCTGTGTAATATGTCTTATAAAC  
AGTTAAAAGCTGAAAAAAAAAAAAAAA

## **FIGURE 30**

MLLLTLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTC SQAQPRG  
EGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

## **FIGURE 31**

TTTGTGAAATTCCCTCAACTATACCCACAGTCAAAAGCAGACTCACTGTGTCCCAGGCTACCAAGT  
CCTCCAAGCAAGTCATTTCCCTTATTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT  
ATTTCGATCTGTTGATAAATGATGTTGACACCCTCACCGAATTCTAAGTGGATCATGTCGG  
GAAGAGAGATAACAATCCTGGCCTGTGTATCCTCGCATTAGCCTGTCTTGGCATGATGTTACC  
TTCAGATTCATCACCAACCCCTCTGGTTCACATTTCATTGGTATTGGGATTGTTGTT  
TGTCTGGGTGTTTATGGTGGCTGATTATGACTATACCAACGACCTCAGCATAGAATTGGACA  
CAGAAAGGAAAATATGAAGTGCCTGCTGGGTTGCTATCGTATCCACAGGCATCACGGCAGT  
CTGCTCGTCTTGATTGGTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTCCAAATCAC  
AAATAAAGCCATCAGCAGTGCCTCCCTGCTGTTCCAGCCACTGTGGACATTGCCATCCTCA  
TTTCTCTGGGTCCCTGGGTGGCTGCTGCTGAGCCTGGAACTGCAGGAGCTGCCAGGTT  
ATGGAAGGCAGGCAAGTGGATATAAGCCCCTTCGGGCATTGGTACATGTGGCGTACCATTT  
AATTGGCCTCATCTGGACTAGTGAATTCATCCTGCGTGCAGCAAATGACTATAGCTGGGAG  
TGGTTACTTGTATTCAACAGAAGTAAAATGATCCTCTGATCATCCCATCCTCGTCTCTC  
TCCATTCTCTTCTTACCATCAAGGAACGTTGTGAAAGGGTCAATTAACTCTGTGGTGA  
GATTCCGAGAACATTGTATGTACATGCAAACGCAGTGAAGAACAGCAGCATGGTCATTGT  
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTCTGGTGTCTGACAAATACCTGCTCCATCTC  
AACCGAGATGCATATACTACAACGTCTATTAACTGGACAGATTCTGTACATCAGAAAAGATGC  
ATTCAAATCTGTCCAAGAACACTCAAGTCACTTACATCTATTAACTGCTTGAGACTTCATAA  
TTTTCTAGGAAAGGTGTTAGTGGTGTTCACTGTTGGAGGACTCATGGCTTTAACTAC  
AATCGGGCATTCCAGGTGTTGGCAGTCCCTGTTATTGGTAGCTTTGGCTACTTAGTAGC  
CCATAGTTTTTATCTGTGTTGAAACTGTGCTGGATGCACCTTCTGTGTTGGCTGATC  
TGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTATGGATCAAGAATTCTGAGTTCGTA  
AAAAGGAGCAACAAATTAAACATGCAAGGGCACAGCAGGACAAGCAGTCAATTAGGAATGAGGA  
GGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTAGGTATCTGTACCTGGAAAACATT  
TCCTTCTAAGAGCCATTACAGAATAGAAGATGAGACCCTAGAGAAAAGTTAGTGAATT  
TTAAAAGACCTAATAACCCATTCTCTCAAAA

## **FIGURE 32**

MSGRDTILGLCILALALSLAMMFTFRFITTLLVHIFISLVLGILFVCGVLWWLYDYTNDSLIE  
LDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTFA  
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQOMTIA  
GAVVTCYFNRSKNDDPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMMQNALKEQQHG  
ALSRYLFRCYCFCWCLDKYLLHLNQNAYTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD  
IIIFLGKVLVVCFVGGLMAFNYNRAFQVWAVPLLVAFFAYLVAHSFLSVFETVLDALFLCFA  
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNAQAQQDKHSLRNEEGTELQAIKR

**Important features:**

**Signal peptide:**

amino acids 1-20

**Putative transmembrane domains:**

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

**N-glycosylation sites.**

amino acids 204-208, 295-299, 313-317

**N-myristoylation sites.**

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

### **FIGURE 33**

GTTCGATTAGCTCCCTGAGAAGAAGAGAAAAGGTTTGGACCTCCTGTTCTTCCTTAGA  
ATAATTTGTATGGGATTGTGATGCAGGAAGCCTAAGGAAAAAGAAATTCAATTCTGTGTTGGT  
GAAAATTTTGAAAAAAAATTGCCTTCTCAAACAAGGGTGTCAATTCTGATATTATGAGGAC  
TGTTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTCCTGTTGCTGGTACTGGAGTAC  
ATTCAAACAAAGAAACGCAAAGAAGATTAAAAGGCCAAGTTCACTGTGCCTCAGATCAACTGC  
GATGTCAAAGCCGAAAGATCATGATCCTGAGTTCAATTGTGAAATGTCAGCAGGATGCCAAGA  
CCCCAAATACCATGTTATGGCACTGACGTGATGCATCCTACTCCAGTGTGTGGCGCTGCCG  
TACACAGTGGTGTGTTGATAATTCAAGGAGGAAAATACTTGTGCGAAGGTTGCTGGACAGTCT  
GGTTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTTATCCCTACCACGATGGAGAGAAATCCTT  
TATCGTCTTAGAAAGTAAACCCAAAAGGGTGTAACTTACCCATCAGCTCTTACATACTCATCAT  
CGAAAAGTCCAGTGCCAAGCAGGTGAGACCAACAAAGCTATCAGAGGGCACCTATTCCAGGG  
ACAACGTGCAAGCAGGGTCACTCTGATGCACTGCTGGCTGTCACTGTAGCTGTGGCCACCCCCAC  
CACCTTGCCAAGGCCATCCCCCTCTGCTGCTCTAACCCAGCATCCCCAGACCACAATCAGTGG  
GCCACAGGAGCCAGGGAGATGGATCTCTGGTCCACTGCCAACCTACACAAGCAGCCAAAACAGGGCC  
AGAGCTGATCCAGGTATCCAAGGCAGATCCTTCAGGAGCTGCCTCCAGAAAACCTGTTGGAGC  
GGATGTCAGCCTGGACTTGTCCAAAAGAAGAATTGAGCACACAGTCTTGGAGCCAGTATCCC  
TGGGAGATCAAACGTCAAATTGACTTGTGTTTTAATTGATGGGAGCACCAGCATTGGCAAA  
CGGCGATTCCAATCCAGAACAGCAGCTCTGCTGATGTTGCCAAGCTTGTGACATTGGCCCTGC  
CGGTCCACTGATGGGTGTTGTCAGTATGGAGACAACCTGTCACTACTTAACTCAAGACAC  
ACACGAATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGACTTCTAAT  
GTAGGTCGGGCCATCTCTTGTGACCAAGAACCTTCCAAAGCAATGGAAACAGAACGG  
GGCTCCAAATGTGGTGGTGGTGTGGGGATGGCTGGCCACGGACAAAGTGGAGGGAGGCTCAA  
GACTTGGAGAGAGTCAGGAATCAACATTCTCATCACCATTGAAGGTGCTGCTGAAAATGAG  
AAGCAGTATGTGGTGGAGCCAACTTGTCAAACAAGGCCGTGTCAGAACAAACGGCTCTACTC  
GCTCCACGTGCAGAGCTGGTTGGCCCTCCACAAGACCCGTGAGCCTCTGGTGAAGCGGGCTGCG  
ACACTGACCGCCTGCCCTGCAGCAAGACCTGCTGAACCTGGCTGACATTGGCTCGTCATCGAC  
GGCTCCAGCAGTGGGGACGGCAACTCCGCACCGTCTCCAGTTGTGACCAACCTCACCAA  
AGAGTTGAGATTCGACACGGACACGCGCATCGGGGGCGTGCAGTACACCTACGAACAGCGGC  
TGGAGTTGGGTTGACAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAAGAGGGTGGG  
TACTGGAGTGGTGGACCAAGCACGGGGCTGCCATCAACTCGCCCTGGAGCAGCTTCAAGAA  
GTCCAAGCCAACAAGAGGAAGTTAATGATCCTCATCACCAGCAGGGAGGTCTACGACGACGCC  
GGATCCCAGCCATGCTGCCATCTGAAGGGAGTGTACACCTATGCGATAGGCCTGCTGGCT  
GCCCAAGAGGAGCTAGAAGTCATTGCACTACCCCGCAGAGACCACCTCTTGTGGACGA  
GTTTGACAACCTCATCAGTATGTCCTCAGGATCATCAGAACATTGTACAGAGTTCAACTCAC  
AGCCTCGGAACCTGAATTCAAGAGCAGGGCAGAGCACCAGCAAGTGTGCTTACTAATGACGTGTT  
GGACCAACCCACCGCTTAATGGGCACGCCAGGGCATCAAGTCTGGCAGGGCATGGAGAAC  
AAATGTCCTGTTATTCTTGCATCATGTTTCAATTCCAAAAGTGGAGTTACAAGA  
TGATCACAAACGTATAAGATGAGCCAAGGCTACATCATGTTGAGGGTGTGGAGATTTCAT  
TTTGACAATTGTTTCAAAATAATGTCGGAATACAGTGCAGGCCCTACGACAGGCTTACGTAG  
AGCTTTGTGAGATTAAAGTGTGTTATTCTGATTTGAACCTGTAAACCTCAGCAAGTTCAT  
TTTGTCATGACAATGTAGGAATTGCTGAATTAAATGTTAGAAGGATGAAAAAATAAAAAAAAA  
AAG

## **FIGURE 34**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG  
CQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSPRWR  
ESFIVLESKPCKKGVTYPSSKSPAAQAGETTKAYQRPIPPTTAQPVTLMQLLAVTVAVA  
TPPTTLPRPSPSAASTTSIPRPQSVDGHRSQEMDLWSTATYTSSQRPRADPGIQRQDPSGAAFQKP  
VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQOLLADVAQALDI  
GPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN  
RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG  
FYSLHVQSWFGLHKTLQPLVKRVCDTDRACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN  
LTKEFEIISDTDTRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKRVGWWSGGTSTGAINFOALEQL  
FKKSCKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAQQEELEVIATHPARDHSFF  
VDEFDNLHQYVPRIIQNICTEFNSQPRN

**Important features:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 181-200

**N-glycosylation sites.**

amino acids 390-394, 520-524

**N-myristoylation sites.**

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,  
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

**Amidation site.**

amino acids 304-308

## **FIGURE 35**

CCGAGCACAGGAGATTGCCTGCCTTAGGAGGTGGCTCGCTGTGGAAAAGCTATCAAGGAAGAAATTGC  
CAAACCATGTCTTTTCTGTTTCAGAGTAGTTACAACAGATCTGAGTGTTAATTAAGCATGGAAT  
ACAGAAAACAACAAAAACTTAAGCTTAATTCATCTGGAATTCCACAGTTCTAGCTCCCTGGACCC  
GGTGACCTGTTGGCTTCCCGCTGGCTCTATCACGTGGTCTCCGACTACTCACCCCGAGTGA  
AAGAACCTTCGGCTCCGCTGCTTGAGCTGCTGGATGGCCTGGCTCTGGACTGTCCTCCGAGTA  
GGATGTCAGTGAGATCCCTCAAATGGAGCCTCGCTGCTGTCACTCCTGAGTTCTTGATGTGGTAC  
CTCAGCCTCCCCACTACAATGTGATAAGAACCGGTGAACGGTACTGAGTTCTATGAGTATGAGCCGATT  
CAGACAAGACTTCACTTCACACTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGA  
GGTGGACCTCCCACCCCTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGA  
TGGTGGGGATATGAGGTCTTACATTTCTTATTAGGCCAAGAGGCTGAAAGAGACAAAATGTTGG  
ATTGTCCTTAGGGATGAACACCTCTTATGGTGAACATAATCCGACAAGATTTTAGACACATATAATA  
ACCTGACCTGAAAACCATTATGGCAATTCAAGGTGGTAACTGAGTTGCCCCATGCCAAGTACGTAATG  
AAGACAGACACTGATGTTTCAACTGGCAATTAGTGAAGTATTTAAACCTAAACCACTCAGA  
GAAGTTTCACAGGTTACCTCTAAATTGATAATTATTCCCTAGAGGATTTACCAAAAAACCCATATT  
CTTACCAAGGAGTATCCTTCAAGGTGTTCCCTCATACTGCAGTGGGTTGGGTATATAATGTCAGAGAT  
TTGGTGCCAAGGATCTATGAAATGATGGTCACGTAACCTGAGTTGAAGATTTATGTCGGGAT  
CTGTTGAATTATTAAAAGTGAACATTCAATTCCAGAAGACACAAATCTTCTTCTATATAGAATCC  
ATTGGATGTCTGTCAACTGAGACGTGATTGCAGCCCAGGCTTCTCCAAGGAGATCATCACTTT  
TGGCAGGTCACTGCAAGGAACACCACATGCCATTTAACTTCACATTCTACAAAAGCCTAGAAGGACAG  
GATACCTGTGAAAGTGTAAATAAAAGTAGGTAAGTGTGTTGAGGACACAAATCTTCTTCTATAGAATCC  
ACACTGAACACTCATGAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTATTAGTCAGG  
CCCTTCAAGATGATGTGGAGGAATTAAATATAAGGAATTGGAGGTTTGCTAAAGAAATTAAATAGG  
ACCAAACAATTGGACATGTCATTCTGTAGACTAGAATTCTTAAAGGGTGTACTGAGTTATAAGCTCA  
CTAGGCTGAAAAACAAACATGTAGAGTTATTGAAACATGTAGTCAGTGAAGGTTTGCTA  
TATCTTATGTGGATTACCAATTAAATATATGTAGTTCTGTGTCAAAAACCTTCACTGAAGTTATA  
CTGAACAAAATTTCACCTGTTGGTCATTATAAGTACTTCAGAATGTGCACTGAGTTTGTGTT  
ATTATTAAAATTACTCAACTTGTGTTTAAATGTTTGACGATTCAATACAAGATAAAAGGATAG  
TGAATCATTCTTACATGCAAACATTCCAGTTACTTAACATGCACTGAGTTTATTGATACATCACTCCA  
TTAATGTAAGTCAGGTCAATTGCAATTCAGTAATCTTGTGACTTTGTTAAATATTACTGTGGT  
AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

## **FIGURE 36**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFVMMWYLSLPHYNVIERVNWMYFYEYEPIYRQDFHF  
TLREHSNC SHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFFLLGQEAEKDMLA  
LSLEDEHLLYGDII RQDFLDTNNNLKTTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYLL  
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRLVPRIYEMMGHV  
KPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR  
NTTCHY

**Important features:**

**Type II transmembrane domain:**

amino acids 20-39

**N-glycosylation sites.**

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

**Glycosaminoglycan attachment site.**

amino acids 239-243

**Ly-6 / u-PAR domain proteins.**

amino acids 23-37

**N-myristoylation site.**

amino acids 271-277

## **FIGURE 37**

CGCTGGGGCACCGCCGCCAAGGGATGGAGCTGGCTGGACGAGTGGGGCTCACTTTCTCAGCTCCTCTCATC  
TCGTCTTCCAAGAGAGTACACAGTCATAATGAAGCTGCCCTGGAGCAGAGTGGAAATATCATGTCGGAGTG  
AATATGATCAGATTGAGTGCCTGCCCGAAGAGGAAGTCTGGTTATACCATCCCTGCTGCAGGAATGAGGAGAA  
TGAGTGTGACTCTGCCATCCACCCAGTTGACCATCTTGAAAAGTCAAGAGCTGCCAAATGGCTATGGGGGGT  
ACCTGGATGACTCTATGTGAAGGGGTTCTACTGTGCAAGAGTGCAGGCCAGGGCTGGTACGGAGGAGACTGCATGCATGTG  
GCCAGGGTCTGCCAGCCCCAAAGGGTCAGATTGTTGAGGAAAGTATCCCCTAAATGTCAGTGTGAATGGACCATTGATGC  
TAAACCTGGGGTTGTCATCCAACTAAGATTGTCATGTTGAGTCTGGAGTTGACTACATGTCCAGTATGACTATGTGAG  
GTTCTGATGGAGACAACCGCGATGGCCAGATCATCAACCGTGTCTGGCAACGAGCGGCCAGCTCTATCCAGAGCATAG  
GATCCTCAGTCACGCCCTTCCACTCCGATGGCTCCAAGAAATTGACGGTTCCATGCCATTATGAGGAGATCACAGC  
ATGCTCCATCCCTGTTCCATGACGGCACGTGCGCTTGACAAGGCTGGATCTACAAGTGTGCCCTGCTGGCAGGC  
TAACTGGCAGCGCTGAAAATCTCTGAAAGAAAGAACCTGCTCAGACCCCTGGGGGCCAGTCATGGTACCAAGAAA  
TAACAGGGGCCCTGGGCTATCAACGGAGCCATGCTAAAATTGGCACCGTGGTGTCTTCTTTGTAACACTCCTATGT  
TCTTAGTGGCAATGAGAAAAGAACCTGCCAGCAGAATGGAGAGTGGTCAGGGAAACAGCCCCTGCTCAAAGCCTGCCGA  
GAACCAAAGATTTCAGACCTGGTGAGAAGGGAGAGTTCTCCGATGCAAGGTTCAAGGGAGACACCAATTACACCAAGCTAT  
ACTCAGCGGCCCTCAGCAAGCAGAAAAGTCAAGAGTGCAGGCCCTACCAAGAAGGCCAGCCCTCCCTTGGAGATCTGCCCTGG  
ATACCAACATCTGCATACCAGCTCCAGTATGAGTGCATCTACCCCTCTACCGCCGCTGGCAGCAGCAGGAGACATGT  
CTGAGGACTGGGAAGTGGAGTGGCGGGCACCATCTGATCCCTATCTGGGAAAATTGAGAACATCACTGCTCCAAAGA  
CCAAGGGTGGCTGGCGTGGCAGGCCATCTACAGGAGGACCAGCGGGGTCATGCGGCACCTACACAAGGGAGC  
GTGGTCTCTAGTCTGCAGCGGTGCCCTGGTAATGAGCGCAGTGTGGTGTGGCTGCCACTGTGTACTGACCTGGGGAG  
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGGGAAATTCTACCGGGATGATGACCGGGATGAGAACGACCATCC  
AGAGCCTACAGATTCTGCTATCATTCTGCATCCAACTATGACCCCATCTGCTGTGACATGCCATCTGAAGCT  
CTTAGACAAGGCCGTATCAGCACCCGAGTCCAGGCCATCTGCCCTGCTGCCAGTCGGGATCTCAGCACCTCCCTCAGGAG  
TCCACATCACTGTGGCTGGCTGGAAATGCTGGCAGACGTGAGGAGCCCTGGCTCAAGAACGACACACTGCGCTCTGGGG  
TGGTCAGTGTGGGGACTCGCTGCTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGTGACTGTACTGATAACATGTT  
CTGTGCCAGCTGGGAAACCACTGCCCTCTGATATCTEACTGCAGAGACAGGAGCATGCCCTGTCCTTCCCCGGG  
CGAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGGTCAAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA  
CTGCCCTCAGGAGTGCCTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGTCATGCCACTCCCTGAGAAG  
TGTGTTCTGTATATCGTCTGTCAGCTGTGTCATGCCGTAAGCAGTGTGGGCTGAAGTGTGATTGGCTGTGAACCTGGCT  
GTGCCAGGGCTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAAGTGAACCTCCATTGCTGGTAGGCTGATGCCGCTCCA  
CTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAGAACAGTAAGTTCTCAAGAACGACCATATACAAAACCTCTCCA  
CTCCACTGACCTGGTGGCTTCCCAACTTCAGTTATGCAATGCCCATCAGCTTGACCAAGGGAGATCTGGCTTCTGAG  
GCCCTTGGAGGCTCTCAAGTCTAGAGAGCTGCCCTGTGGAGCACCCAGGGCAGCAGAGCTGGGATGTGGCTCATGCC  
TGTGACATGGGCCAGTACAGTCTGGCTTTCTCCCATCTTGTACACATTAAATAAAATAAGGGTGGCTTCT  
GAACTACAA  
AA

## **FIGURE 38**

MELGCWTQLGLTFLQLLISSLPREYTVINEACPGAEWNIMCRECCYEVDQIECVCPGKREVVGYT  
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWGGDCMRCGQ  
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGQII  
KRCVGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC  
ACLAGYTQRCENLLEERNCSDPGGPVNGYQKITGGPGILINGRHAKIGTVVSFFCNNSYVLSGNE  
KRTCQQNGEWSGKQPICIKACREPDKISDLVRRRLPMQVQSRETPHLQLYSAAFSKQKLQSAPTK  
KPALPFGLPMGYQHLHTQLQYECISPFYRRLGSSRTCLRTGKWSGRAPSCIPICGKIENITAP  
KTQGLRLWPWQAAIYRRRTSGVHDGSLHKGAFLVCGALVNERTVVVAHCVTDLGKVTMIKTADL  
KVVLGKFYRDDRDEKTIQSLQISAIILHPNYDPILLADIAILKLLDKARISTRVQPICLAASR  
DLSTSFQESHITVAGWNVLADVSPGFKNDSLRSGVSVVDSLLCEEQHEDHGIPVSVDNMFCA  
SWEPTAPSIDIETGGIAAVSFGRASPEPRWHLMGLVWSYDKTCSHRLSTAFTKVLPKDWI  
ERNMK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**EGF-like domain cysteine pattern signature.**

amino acids 260-272

**N-glycosylation sites.**

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

**N-myristoylation sites.**

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
474-480, 491-497, 638-644, 666-672

**Amidation site.**

amino acids 56-60

**Serine proteases, trypsin family.**

amino acids 489-506

**CUB domain proteins profile.**

amino acids 150-167

### **FIGURE 39**

GGTCTCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTACGGGCCGTGATTATTAACGTGGCTTAATC  
TGAAGGTTCTCAGTCAAATTCTTGTGATCTACTGATTGTTGGGGCATGGCAAGGTTGCCTAAAGGAGCTGGCTG  
TTTGGGCCCTGTAGCTGACAGAAGGTGCCAGGGAGAATGCAGCACACTGCTCGAGAATGAAGGCGCTCTGTTG  
TGGTCTTGCTGGCTCAGTCCTGCTAATCATTGACAATGTGGCAACCTGCACITCCTGTATTCAAACTCTGTA  
AAGGTGCCCTCCACTACGGCCTGACCAAAGATAGGAAGAGGCCCTACAAGATGGCTGCCAGACGGCTGTGAGGCC  
TCACAGGCCAGGGCTCCCTCCCCAGAGGTTCTGCAGTGCCACCATCTCTTAATGACAGACGAGCCTGGCTAGAC  
ACCCCTGCCCTACGTGCTCGGAGGGACGGGAGCCAGCAATCAGCCCAGTGACTCTGGCCAGGCAACCGA  
GGGCACGGCCCTTGAGAGATCCACTATTAGAACGAGATCATTAAAAAAATAAATCGAGCTTGAGTGTCTCGA  
GGACAAAGAGCGGGAGTGCAGTTGCAACCATGCCGACCAGGGCAGGGAAATTCTGAAAACACCAACTGCCCTGAAG  
TCTTCCAAGGTTGACACCTGATTCCAGATGGTGAATTACAGCATCAAGATCAATCGAGTAGATCCAGTGA  
GCCTCTCTATTAGGCTGGGGAGGTAGCAGAACCCACTGGTCCATATCATTATCAACACATTATCGTGA  
TGATGCCAGAGACGCCGCTACTGCCAGGAGACATCATTCTAAAGGTCAACGGATGGACATCAGCAATGCTC  
ACAACACTACCGCTGCGTCCCGCCAGGCTGCCAGGTGCTGACTGTGATCGTGAACAGAAGTCCCGA  
GCAGGAACATGGACAGGCCCGATGCCATCACAGACCCAGATGACAGCTTCATGTGATTCTAACAAAAGTAGCC  
CCGAGGAGCAGCTGGAAATAAACTGGTGCAGGAGACATCATTCTAAAGGTCAACGGATGGACATCAGCAATGCTC  
GTGTGGCATATCGACATGGTCAGCTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTCGATATGGCA  
GCCAGAAAGTGCCTCATCTGATTCAAGGCCAGTGAAGACGCTTCACCTCGTGTGCCAGGTGGCAGC  
GGAGCCCTGACATCTTCAGGAACCCGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCAGGGAGAGGCA  
CTCCCAAGCCCTCCATCTACAATTACTGTGATGAGAAGGTGTAATACCAAAAGACCCGGTGAATCTCTG  
GCATGACCGTGCAGGGAGCATTACAGAGAATGGGATTTGCATCTATGTCATCAGTGTGAGCCGGAGGAG  
TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTGTTGAATGTGGATGGGCGAACTGACAGAGGTGAGCC  
GGAGTGAGGCGAGTGGCATTATTGAAAAAGAACATCATCCTCGATAGTACTCAAAGCTTGGAAAGTCAAAGAGTATGAGC  
CCCAGGAAGACTGCAGCAGGCCAGCAGGCCCTGGACTCCAACCACACATGGCCCAACCCAGTGA  
CTGGTCCCACATGGTGAATGGGCTGGCATATTACCGGTGCTGTATAACTGTAAGAGTATTGTTACAGA  
TGGGCTCTGCATTGTAGGAGGTTATGAGAAGAATACAATGGAAACAAACCTTTTCACTCAATCATTGTTGA  
CACCAGCATACAATGATGAGAAGAATTAGATGTGGTGAATTCTCTGCTGCAATGGTAGAAGTACATCAGGA  
TACATGCTTGTGAGACTGCTGAAAGAACCTAAAGGAGAAATTACTCTAACATTTGTTCTGGCTGGCA  
TTTTTAGAATCAATGATGGGTCAGAGGAAACAGAAAAATCACAATAGGCTAAGAAGTGAAAACACTATATTATC  
TTGTGAGTTTATATTAAAGGAGAATACATTGAAAAATGTCAAGGAAAGTATGATCATCTAACATGAA  
ACACCTCAGAAAATATGATTCCAAAAAAATTAAACACTAGTTTTTCAGTGTGGAGGATTCTCATTACTCTAC  
AACATTGTTTATATTCTATTCAATAAAAAGCCCTAAACAAACTAAATGATTGATTTGTATACCCACTGA  
CAAGCTGATTAAATTAAAATTGGTATATGCTGAAGTCTGCCAAGGGTACATTATGCCATTAA  
AAAAATTTTAAATGCTGAGAAACGTTGCTTTCATCAAACAAAGAATAAATTTTCAAGGTTAA

## **FIGURE 40**

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPDGCASLTATAPS  
PEVSAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDGRSNRTRARPFERSTIRSRSFKKINR  
ALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVPSESLSIRLV  
GGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM  
REQKFRSRNNGQAPDAYPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVIFNVLDGGVAYRHG  
QLEENDRVLALINGHDLRYGSPEAAHLIQASERRVHLVSRQRSPDIFQEAGWNSNGSWSPG  
PGERSNTPKPLHPTTCHEKVVNICKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDRGR  
IKTGDILLNVDGVELTEVSERSEAVALLKRTSSIVLKALEVKYEPOQEDCSSPAALDSNHNMAPP  
SDWSPSWMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG  
RIRCQDILLAVNGRSTSGMIHACLRLLKELKGRITLTIVSWPGTFL

**Important features:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-112, 157-161, 289-293, 384-388

**Tyrosine kinase phosphorylation sites.**

amino acids 433-441, 492-500

**N-myristoylation sites.**

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,  
467-473, 603-609

## **FIGURE 41**

ACCAAGGCATTGTATCTCAGTTGTCATCAAGTTCGAATCAGATTGGAAAAGCTCAACTGAAGCTT  
CTTGCCCTGCAGTGAAGCAGAGAGATAGATAATTACAGTAATAAAACATGGGCTCAACTGACT  
TTCCACCTTCTACAAATTCCGATTACTGTTGCTGTTGACTTGTGCTGACAGTGGTTGGGTGGC  
CACCAAGTAACACTTCGTGGGTGCCATTCAAGAGATTCTAAAGCAAAGGAGTTCATGGCTAATTCC  
ATAAGACCCCTCATTGGGAAGGGAAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACCT  
GACAACGTCCCTGTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTCAAACCAGATCTCAC  
TTTGGAAAGAGGTACAGGCAGAAAATCCAAAGTGTCCAGAGGCCGTATGCCCTCAGGAATGTAAG  
CTTACAGAGGGTCGCCATCCTCGTTCCCCACCGAACAGAGAGAAACACTGTACCTGCTGGAA  
CATCTGCATCCCTCCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCTACCCAGGCTGAAGG  
TAAAAAGTTAATCGAGCAAACCTTGAATGTGGCTATCTAGAACGCCCTCAAGGAAGAAAATTGGG  
ACTGCTTATATTCCACGATGTGGACCTGGTACCCGAGAACTGACTTTAACCTTACAAGTGTGAGGAG  
CATCCCAAGCATCTGGTGGTGGCAGGAACAGCACTGGTACAGGTTACAGTGGATATTGG  
GGGTGTTACTGCCCTAACGAGAGCAGTTTCAGGTGAATGGATTCTCTAACAAACTACTGGGAT  
GGGGAGGCGAACAGCATGACCTCAGACTCAGGGTTGAGCTCCAAAGAACATGAAAATTCCCGCCCCCTG  
CCTGAAGTGGTAAATATAACATGGCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG  
GATGAAGCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGTTGAGTAGTTCTTGTATTAAT  
TAGTATCTGTGGAACACAATCCTTATATATCACACATCACAGTGGATTCTGGTTGGTGCATGACCC  
TGGATCTTGGTGTGTTGGAAGAACTGATTCTTGCAATAATTGGCCTAGAGACTTCAA  
ATAGTAGCACACATTAAGAACCTGTTACAGCTATTGTGAGCTGAATTTCCTTTGTATTTCT  
TAGCAGAGCTCTGGTGTGAGTAAACAGTTGTAACAAGACAGCTTCTTAGTCATTGAT  
CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTATATAAAAGGATGACTCAAAGGATAA  
AATGAACGCATTTGAGGACTCTGGTGAAGGAGATTATTAAATTGAGTAATATATTGGGAT  
AAAAGGCCACAGGAATAAGACTGCTGAATGCTGAGAGAACAGAGTTGTTCTCGTCCAAGGTAGAA  
AGGTACGAAGATAACAAACTGTTATTCAATTCTGTACAATCATCTGTGAAGTGGTGGTGTAGGT  
GAGAAGGGTCCACAAAAGAGGGAGAAAAGGCAGAACAGGACACAGTGAACCTGGGATGAAGA  
GGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC  
CTTCAGGGGAGGACCTGCCAGGTATGCCCTCAGTGTGAGCTGGTGCAGGTGCTGATAGC  
TTTAAAGAGTTTGAAAATGATTGTACAAGTAGGATATGAATTAGCAGTTACAAGTTACAT  
ATTAACATAATAATATGTCTACAAACCTCTGTAGTAAAGTGAAGCAAA

## **FIGURE 42**

MGFNLTFHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLGKGKTLTN  
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH  
RNREKHILMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFIFHDV  
DLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGTALSREQFFKVNGFSNNYWGWGGED  
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQSVRVRTDGLSSCSYKLV  
SVEHNPLYINITVDFWFGA

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**

amino acids 191-202

### **FIGURE 43**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCATGAGCTCCAGATCTGGG  
CCGCTTGCCTCCTGCTCCTCCTCCTGCCAGCCTGACCAGTGGCTCTGTTCCCACAACAG  
ACGGGACAACTTGCAGAGCTGCAACCCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCAT  
GTTCCAGAGGCGAAGGAGGCAGACACCCACTCCCCATCTGCATTTCGCTGCGGCTGCTGTC  
ATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCGTCCCCTCCC  
TTCCTTATTATTCTGCTGCCAGAACATAGGTCTTGAATAAAATGGCTGGTTCTTGTT  
TCCAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELOPQDRAGARASWMPMFQRRRRDTHFPI  
CIFCCGCCHRSKCGMCKT

**Important features:**

**Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 58-59

**N-myristoylation site.**

amino acids 44-50

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 1-12

## **FIGURE 45**

GTGGCTTCATTCAGTGGCTGACTCCAGAGAGCAATATGGCTGGTCCCCAACATGCCTCACCC  
TCATCTATATCCTTGCGAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT  
TCCGTTGGTGGGCCGTGACTTCCCCCTGAAGTCAAAGTAAAGCAAGTTGACTCTATTGTCTG  
GACCTCAACACAACCCCTCTTGTACCATAACGCCAGAAGGGGGCACTATCATAGTGACCCAAA  
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAACGTGAAG  
AAGAATGACTCAGGGATCTACTATGTGGGATATAACAGCTCATCACTCCAGCAGCCCTCCACCCA  
GGAGTACGTGCTGCATGTCTACGAGCACCTGCTCAAAGCTAAAGTCACCATGGTCTGCAGAGCA  
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATT  
TATACCTGGAAGGCCCTGGGCAAGCAGCCAATGAGTCCCATAATGGTCCATCTCCCCATCTC  
CTGGAGATGGGAGAAAGTGATATGACCTTCATCTGCCTGCCAGGAACCTGTCAGCAGAAACT  
TCTCAAGCCCCATCCTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATG  
GTCCTCTGTGTCTCCTGTTGGTCCCCCTCTGCTCAGTCTCTTGTACTGGGGCTATTCTTG  
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTGTCGGG  
AAACTCTAACATATGCCCTATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT  
AGAACAACTCTAACAGAACATCCCTGCTCACGATGCCAGACACACCAAGGCTATTGCCTATGAGAATGTTA  
TCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCA

## **FIGURE 46**

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLSKVKQVDSIVWTFTTPLVTIQP  
EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK  
PKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC  
VARNPVSRNFSSPIILARKLCEGAADDPDSSMVLLCLLLVPLLLFLVGLFLWFLKRERQEEYIE  
EKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT  
PRLFAYENVI

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 224-250

**Leucine zipper pattern.**

amino acids 229-251

**N-glycosylation sites.**

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,  
291-295

## **FIGURE 47**

GGCTCGAGCGTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGG  
ATTCAGCCTGCTGGTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATAACCTCTAATTGTCAGCT  
TAGTTGAGGAAGACCAATTTCTCAAAACCCCATCTTGCTTGAGTGGTGGTCCCAGGAATT  
ATAGGAGCAGGTCTGATGCCATTCCAGCAACAACAATGCTTGACAGCAAGAAAAAGAGCGTG  
CTGCAACAAACAGAACTGGAATGTTCTTCATCATTTTCAGTGTGATCACAGTCATTGGTGCTC  
TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCTCATGTGTAATTCTCCAAGC  
AACAGTAATGCCAATTGTGAATTTCATTGAAAAACATCAGTGACATTCATCCAGAATCCTCAA  
CTTGCAGTGGTTTCAATGACTCTTGTGCACCTCCTACTGGTTCAATAAACCCACCAGTAACG  
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTCCACTCGATTCTGAAGAAAACAAACATAGG  
CTTATCCACTCTCAGTATTTAGGTCTATTGCTTGGAATTCTGGAGGTCTGTTGGC  
CAGTCAGATAGTCATCGGTTCCCTGGCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG  
TGTAGTTAATGGGAATAAAATGTAAGTATCAGTAGTTGAAAAAAAAAA

## **FIGURE 48**

MTCCEGWTSCNGFSLLVLLLGVVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA  
TTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNANCEFSL  
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGL  
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

**Important features:**

**Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

**N-glycosylation sites.**

amino acids 80-84, 132-136, 148-152, 163-167

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 223-227

**N-myristoylation sites.**

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 207-218

**TNFR/NGFR family cysteine-rich region protein.**

amino acids 4-12

## **FIGURE 49**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTGCCAAGGTGACCTCGCAGGACACTGGTGA  
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG  
ATCCGTGGGCTGCAGACCCCCGCCAGTGCCTCTCCCCCTGCAGCCTGCCCTCGAACTGTGA  
CATGGAGAGAGTGACCCCTGGCCCTCTCCTACTGGCAGGCCTGACTGCCTTGGAGCCAATGACC  
CATTTGCCAATAAACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC  
TGCAGGGCTCCTGGCATTGCTGGATCGCGCAGTTCTGAGTGGCAAATGCAAATACAAGAG  
CAGCCAGAACGAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA  
CTACTTGCTGAGCACAGGACTGCCCTCCAGGGATGCCCTGAAGCCTAACACTGCCAGCACC  
TCCTCCCCCTGGAGGCCTTATCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCT  
TTCTGATCAGGAGGCTTCTTATGAATTAAACTCGCCCCACCACCCCTCA

## **FIGURE 50**

MERVTLALLLLAGLTALLEANDPFANKDDPYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS  
SQKQHSPVPEKAIPPLITPGSATTC

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 36-59

**N-myristoylation sites.**

amino acids 41-47, 45-51, 84-90

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.**

amino acids 54-67

## **FIGURE 51**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG  
AGGACAGGGAGTCGAAGGAGGAGCACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGCAAGG  
AGGAGACCTGGTGGGAGGAAGACACTCTGGAGAGAGAGAGGGGCTGGCAGAGAATGAATTCCAG  
GGGCCCTGGCCTGCCTCCTGCTGGCCCTCTGCTGGCAGTGGGAGGCTGGCCCTGCAGAG  
CGGAGAGGAAAGCACTGGACAAATATTGGGAGGCCCTGGACATGGCCTGGAGACGCCCTGA  
GCGAAGGGTGGAAAGGCCATTGGCAAAGAGGCCGGAGGGCAGCTGGCTCTAAAGTCAGTGAG  
GCCCTGGCCAAGGGACCAGAGAACAGCTGGCACTGGAGTCAGGCAGGTTCCAGGTTGGCGC  
AGCAGATGCTTGGCAACAGGGTGGGAAGCAGCCCAGTCTGGAAACACTGGGACAGAGA  
TTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCAGATGCTGTCGGCTCCTGGCAGGG  
GTGCCTGGCCACAGTGGTCTGGAAACTCTGGAGGCCATGGCATCTTGGCTCTCAAGGTGG  
CCTTGGAGGCCAGGGCAATCCTGGAGGTCTGGGACTCCGTGGTCCACGGATAACCCCG  
GAAACTCAGCAGGCCAGTGGAAATGAATCCTCAGGGAGCTCCCTGGGTCAGGAGGCAATGG  
GGGCCACCAAACCTTGGACCAACACTCAGGGAGCTGGCCCAGCCTGGCTATGGTCAGTGAG  
AGCCAGCAACCAGAATGAAGGGTGCACGAATCCCCCACCCTGGCTCAGGTGGAGGCTCCAGCA  
ACTCTGGGGAGGCAGCGCTCACAGTCGGCAGCAGTGGCAGCAGCAGTGGCAGCAGTGGCGCAGCAG  
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGTGGCAGCAGCAGTGGCAGCAGTGG  
TGGCGCAGCAGTGGTGGCAGCAGTGGCAGCAGTGGCAGCAGGAGGTGACAGCGCAGTGA  
CCTCCTGGGATCCAGCACCGGCTCCTCCGGCAACCACGGTGGAGCGGGAGGAAATGG  
CATAAACCCGGGTGTGAAAGCCAGGGAAATGAAGCCCGGGAGCAGGGAAATCTGGGATTCA  
CTTCAGAGGACAGGGAGTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATGCCCTTG  
GAGGCTCTGGAGACAATTATCGGGGCAAGGGTCGAGCTGGGAGTGGAGGAGGTGACGCTTT  
GGTGGAGTCATACTGTGAACCTCTGAGACGTCTGGATGTTAACCTTGACACTTCTGGAA  
GAATTTAAATCCAAGCTGGTTTCATCAACTGGGATGCCATAAACAAAGGACCAGAGAAGCTC  
GCATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGAGGCCACACTCCCTCTAA  
AACACCAACCCCTCTCATCACTAACTCAGCCCTGGGATGAAATAACCTTAGCTGCCCAACAAA  
AA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 52**

MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVS  
EALGQGTREAVGTGVRQVPGFAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGVP  
GHSGAWETSGGHGIFGSQGGLGGQQGQGNPGLGTPWVHGYPGNSAGSFGMNPQGAPWGQGGNGPPNF  
GTNTQGAVAQPGYGSVRASNQNEGCTNPPSGSGGGSSNSGGSGSQSGSSGSGSNGDNNNGSSSGS  
SSGSSSSGSSGGSSGGSSGSSGSGSRGDSGSESSWGSSTGSSSGNHGGSGGGNGHPGCEKPGNE  
ARGSGESGIQGFRGQGVSSNMREISKEGNRLIGGSGDNYRGQGSSWGSGGDAVGGVNTVSETSPGM  
FNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,  
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,  
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,  
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,  
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,  
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,  
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,  
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,  
387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

## **FIGURE 53**

GGAGAAAGAGGTTGTGGGACAAGCTGCTCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG  
CTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGCTCCTGGCT  
ACTCGCCCGCATCCTGGCTTGGACCTATGCCCTCTATAACAACTGCCGCCGGCTCCAGTGTTCC  
CACAGCCCCAAAACGGAACTGGTTTGGGGTACCTGGGCTGATCACTCCTACAGAGGAGGGC  
TTGAAGGACTCGACCAGATGTCGGCCACCTATTCCAGGGCTTACGGTATGGCTGGTCCCCAT  
CATCCCCTCATCGTTTATGCCACCCTGACACCATCCGGTCTATCACCAATGCCTCAGCTGCCA  
TTGCACCAAGGATAATCTCTTCATCAGGTTCCTAAGGCCCTGGCTGGAGAAGGGATACTGCTG  
AGTGGGGTGACAAGTGAGGCCACCGTCGGATGCTGACGCCGGCTTCCATTCAACATCCT  
GAAGTCCTATATAACGATCTCAACAAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG  
CCTCAGAGGGCAGCAGTCGCTGGACATGTTGAGCACATCAGCCTCATGACCTGGACAGTCTA  
CAGAAATGCATCTCAGCTTGACAGCCATTGTCAGGAGGGCCAGTGAATATATTGCCACC  
CTTGGAGCTCAGTGCCCTGTAGAGAAAAGAACGCAAGCATATCTCCAGCACATGGACTTCTGT  
ATTACCTCTCCCATGACGGGCGGCCTTCCACAGGGCTGCCCTGGTGCATGACTCACAGAC  
GCTGTCATCCGGAGCGGCGTCGCACCCCTCCCCACTCAGGGTATTGATGATTTTCAAAGACAA  
AGCCAAGTCCAAGACTTGGATTCATTGATGTGCTGCTGAGCAAGGATGAAGAGATGGAGG  
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTGGAGGCCATGACACCACG  
GCCAGTGGCCTCTCTGGTCTGTACAAACCTTGCGAGGCACCCAAGAATACCAGGAGCGCTGCCG  
ACAGGAGGTGCAAGAGCTCTGAAGGACCGCGATCCTAAAGAGATGAATGGACGACCTGGCC  
AGCTGCCCTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCTTCATC  
TCCCGATGCTGCACCCCAGGACATTGTTCTCCAGATGGCGAGTCATCCCCAAAGCATTACCTG  
CCTCATCGATATTAGGGTCCATCACAACCCAACTGTGTTGGCCGGATCCTGAGGTCTACGACC  
CCTTCCGCTTGACCCCAGAGAACAGCAAGGGAGGTCACCTCTGGCTTTATTCCCTTCTCGCA  
GGGCCCAGGAACTGCATCGGGCAGGCTTCGCCATGGGGAGATGAAAGTGGTCTGGCGTTGAT  
GCTGCTGCACTTCCGGTCTGCCAGACCACACTGAGCCCCGCAGGAAGCTGGAATTGATCATGC  
GCGCCGAGGGCGGGCTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCAGTGACTTCTGAC  
CCATCCACCTGTTTTTGCAGATTGTCATGAATAAAACGGTGCTGTCAAA

## **FIGURE 54**

MSLLSLPWLGRLRPVAMSPWLLLLVVGSWLLARI LAW TYAFYNNCRRLQCFPQPPKRNWFWGHLG  
LITPTEEGLKDSTQMSATYSQGFTVWLGPPIIPFIVLCHPDTIRSITNASAAIAPKDNL FIRFLKP  
WLGEGLLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSAANIMLDKWQHLASEGSSRLDMFEHI  
SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSDGRRFHRC  
RLVHDFTDAVIRERRTLPTQGIDDFFKDKAKSKTLDFIDVLLSKDEDGKALSDEDIRAEADTF  
MFGGHDTTASGLSWVLYNLRHPEYQERCRCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR  
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHNPTVWPDPPEVYDPFRDPENSKGRSP  
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN  
VGLQ

**Important features:**

**Transmembrane domains:**

amino acids 13-32 (type II), 77-102

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 461-471

**N-glycosylation sites.**

amino acids 112-116, 168-172

## **FIGURE 55**

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTGA  
GCCTACTCGTTGATTGCAACTATCATGGTGTGTTGCACTTACCCGTGTTCTGCCT  
TTTGGTGGCATAACAAGGGACTTGCACTTATCTCTGCATTTGCAGTCTTGCATTGACGTGG  
TACAGCCTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTGCCGTGCTTGC  
ATAATTCATGGCCAGTTTATGAAGCCTTGAAGGCACATGGACAGAAGCTGGTGGACAGTTT  
GTAACTATCTCGAACCTCTGTCTTACAGACATGTGCCTTTATCTTGCAGCAATGTGTTGCTT  
GTGATTGAAACATTGAGGGTTACTTTGAAAGCAACAATACATTCTCGAACCTGAATGTCAGTA  
GCACAGGATGAGAAGTGGTTCTGTATCTTGTGGAGTGAATCTTCTCATGTACCTGTTCTC  
TCTGGATGTTGTCCCAGTAATTCCCATGAATACAAACCTATTCAAGAACAGCAAAAAAAAAAAAA  
AAA

## **FIGURE 56**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCASFWWHNKGALIFCIOSLALTWYSLSFIPFAR  
DAVKKCFAVCLA

**Important features:**

**Signal peptide:**

amino acids 1-33

**Type II fibronectin collagen-binding domain protein.**

amino acids 30-72

## **FIGURE 57**

CGGCTCGAGCTCGAGCCGAATGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCAACATGCTCTGTGCCCTG  
TACGTGCCGTCACTGGGAAGCCCAGACCGAGTCAGACTTTAGTCAGAAGGGCTCCCTGCCAGCTGAAAGTCC  
ATTTCAGCTCATGTCCTCATCCCCCTCCAGGAATTCTCACCTACCGCCAGTGGAGCAGAAAATTGTACAAGCT  
GGAGATAAGGACCTTGATGGCAGCTAGACTTTGAAGAATTGTCATTATCTCAAAGATCATGAGAAGAGCTGAGG  
CTGGTGTAAAGATTGGAAAAAAGAATGATGGACGATTGACCCGAGGAGATCATGCAGTCCCTGCCGGACTTG  
GGAGTCAGATATCTGAAACAGCAGGAGAAAAATTCTCAAGAGCATGGATAAAAACGGCACGATGACCATGACTGG  
AACGAGTGGAGAGACTACCACCTCCACCCCGTGAAAACATCCCGAGATCATCCTACTTGAAGCATTCCACG  
ATCTTGATGTTGGTGAAGAATCTAACGGTCCGGATGAGTTACAGTGGAGGAGGGAGACGGGGATGTGGTGGAGA  
CACCTGGTGGCAGGAGGGGGCAGGGGGTATCCAGAACCTGCACGGCCCCCTGGACGGCTCAAGGTGCTCATG  
CAGGTCCATGCCCTCCCGAGAACAAACATGGGATCGTTGGTGGCTACTCAGATGATTGAGAAGGGAGGGCCAGG  
TCACTCTGGCGGGCAATGGCATCAACGTCCTCAAATTGCCCGAATCAGCCATCAAATTGCGCTATGAGCAG  
ATCAAGGCCCTGTTGGTAGTGGCAGGAGACTCTGAGGATTCAAGAGAGGCTGTGGCAGGGCTTGGCAGGGCC  
ATCGCCCAAGCAGCATCTACCAATGGAGGTCTGTGAAAGACCCGGATGGCGCTGCCAGACGGCAGTACTCAGGA  
ATGCTGGACTGCCAGGAGGATCTGGCCAGAGGGGGTGGCCCTTACAAAGGCTATGCCCCAACATGCTG  
GCCATCATCCCTATGCCGATCGACCTTGCACTACAGAGACGCTCAAGAATGCCCTGCCGACTATGCACTG  
AACAGCCGGACCCGGCTGTTGCTCTGCCCTGTGGCACCAGTCCAGTACCTGTGGCAGCTGCCAGCTAC  
CCCCCTGGCCCTAGTCAGGACCCGGATGCGAGCGCAAGCCTTATTGAGGGCGCTCCGGAGGTGACCATGAGCAGCCTC  
TTCAAAACATATCTCGGACCCAGGGGCTTCCGGCTGTACAGGGGCTGCCAACCTTCAATGAGGTCACTCCA  
GCTGTGAGCAGCATCGACTGGTCTACAGAGAACCTGAGAAGATCACCTGGCGTGCAGTGGCTGAGGGGGGG  
GCCCGGAGTGGACTCGCTATCTGGCCCGCAGCTGGGGTGTGGCAGCCATCTATTGTGAATGTGCCAACACT  
AACAGTGTCTCGAGCCAAGCTGTGAAAACCTAGACGCAACCGCAGGGAGGGTGGGAGAGCTGGCAGGCCAGGGCTT  
GTCCCTGCTGACCCAGCAGACCCCTCTGTTGGTCCAGCGAAGACCAACAGGCACTCTTAGGGTCCAGGGTCA  
CTCGGGGCTCACATGTAAGGACAGGACATTTCGCACTGCTGCCAATAGTGGAGCTGGAGGCTGGAGGGGG  
TAGTTCTTCATCTGGCTGAGCAGCTGGGGCCCTGCCCTCTGGCTGTGGCTGCACTCTGGCTGTGCATCT  
CCTCTGCTGCCCTGCTGAGGTAAGGTGGAGGGGCTCAGGCCACATCCCCACCTCGTCAATCCC  
ATAATCCATGATGAAAGGTGAGGTACGTTGGCTCCAGCCTGACTTCCAACTACAGCAATTGACGCCACTGGC  
TGTGAAGGAAGAGGAAGGGATGCGCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGCTCTGGG  
CTTGGGAGTGCAGGGGCTCGGGCTGCCCTGGCTGACAGAAGGCAAGTGCCTGGGCTCATGGCTCTGAGCT  
GCCCTGGACCCCTGTCAGGATGGGCCCCACCTCAGAACAAACTCACTGTCCCCTGTCATGGGAGTGGAGCA  
CCATGTTGAGGGCAAGGGCAGAGCGTTGTGTTCTGGGGAGGGAGGGAGGGCTTGGAGGCTTAATTATGG  
ACTGTTGGAAAAGGGTTTGTCCAGAAGGACAAGCCGACAATGAGCAGTCTGTGCTTCCAGAGGAAGACGAGG  
GAGCAGGAGCTGGTCACTGCTCAGACTGTTCTGACGCCCTGGGGTCTGCAACCCAGCAGGGGCCAGC  
GGGACCAAGCCACATTCCACTGTCAGCTGGCACTTATTGTTGTTATTGAAACAGAGTTATGCT  
AACTATTATGATGTTAATTAAATGCTTCAAGTCTGCTATTGTTATTGATATTGTTCAATTGTT  
GATTGTACCTTCCAAGCCGCCAGTGGATGGGAGGGAGGAGGAGAAGGGGGCCTTGGCCGCTGCACTCACATCT  
GTCCAGAGAAATTCTTGGACTGGAGGCAGAAAAGCCGCCAGAGGCAACGCCCTGGCTCTTCTGGCAG  
GTTGGGAGGGCTGCCCTAGCCTAGGATTTCAGGGTTGACTGGGGCGTGGAGAGAGAGGGAGGAACCTCAAT  
AACCTTGAAAGGTGGAATCCAGTTATTCTGCGCTGCCAGGGTTCTTATTCACTCTTCTGAATGTCAGGGCAG  
TGAGGTGCTCTCACTGTAATTGTTGTTGGGAGGGGGCTGGAGGGAGGGGGCTGGCTCCGCTCCGCCAGC  
CTTCTGCTGCCCTGCTTAACAAATGCCGCCAACCTGGCACCTCACGGTTGCACTTCCATTCCACCAAAATGACCTGA  
TGAGGAATCTCAATAGGATCAGAACATCAATGAAAATTGTTATATGAAACATATACTGGAGTCGTC  
CAAATTAAGAAGAATTGGACGTTAGAAGGTGTCATTAAAGCAGCTTAATAAGTTGTTCAAAGCTGAAAAAA  
AA

## **FIGURE 58**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVIFPSQEFSTYRQWKQKIVQAGDKDLDG  
QLDFEEFVHYLQDHKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMDKNG  
TMTIDWNEWRDYHLLHPVENIPEIIILYWKHSTIFDVGENLTVPDEFTVEERQTGMWWRHLVAGGG  
AGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIK  
FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARR  
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSADPGVFVLLACGTMSSTC  
GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV  
VYENLKITLGVQSR

**Important features:**

**Signal peptide:**

amino acids 1-16

**Putative transmembrane domains:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation sites.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

## FIGURE 59

GGAAGGCAGCGGCACTCAGGCCAGTACCCAGATAACGCTGGAAACCTCCCCAGCCATGGC  
TTCCCTGGGGCAGATCCTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG  
CACTCATATTGGCTTGGTATTCAGGGAGACACTCCATCACAGTCACTACTGTGCCTCAGCT  
GGGAACATTGGGAGGATGGAATCCTGAGCTGACTTTGAACCTGACATCAAACCTTCTGATAT  
CGTGATACAATGGCTGAAGGAAGGTGTTAGGCTTGGCATGAGTCAGGAAAGGCAAAGATG  
AGCTGTCGGAGCAGGATGAAATGTTAGGCGGACAGCAGTGTGCTGATCAAAGTGTAGTT  
GGCAATGCCCTTTGCGGCTGAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT  
CATCACTCTAAAGCAAGGGGATGCTAACCTTGAGTATAAAACTGGAGCCTCAGCATGCCGG  
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCAGGTGAGGCTCCCGATGGTCCCC  
CAGCCCACAGTGGTCTGGGCATCCAAAGTGTGACCAGGGAGCCAACCTCTCGGAAGTCTCCAATAC  
CAGCTTGAGCTGAACCTGAGAATGTGACCATGAAGGTTGTCTGTGCTCTACAATGTTACGA  
TCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG  
ACAGAACATGGAGATCAAAAGGGAGTCACCTACAGCTGCTAAACTCAAAGGCTCTGTGTT  
CTCTTCTTCTTGCATCAGCTGGCACTCTGCCTCTCAGCCCTACCTGATGCTAAATAAAT  
GTGCCCTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTCAC  
CACCAGATATGACCTAGTTTATATTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG  
AGCAAACAAAGAGCAAGAACAAAAAGAAGCAGAACAGGCTCCAATATGAACAAAGATAAA  
CTATCTCAAAGACATATTAGAAGTTGGGAAAATAATTGATGTGAACTAGACAAGTGTGTTAAGA  
GTGATAAGTAAAATGCACGTGGAGACAAGTGCATCCCAAGATCTCAGGGACCTCCCCCTGCCTGT  
CACCTGGGAGTGAAGAGGACAGGATAGTGCATGTTCTGTCTGAAATTAGTTATATGTGC  
TGTAATGTTGCTCTGAGGAAGCCCCTGAAAGTCTATCCAAACATATCCACATCTTATATTCCAC  
AAATTAAAGCTGTAGTATGTACCCCTAAGACGCTGCTAATTGACTGCCACTCGCAACTCAGGGCG  
GCTGCATTTAGTAATGGGTCAAATGATTCACTTTTATGATGCTTCAAAGGTGCCTGGCTTC  
TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTAGCATAAACAGAGCAGT  
CGGGGACACCGATTATAAAACTGAGCACCTTCTTTAAACAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 6o**

MASLGQILFWSIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS  
DIVIQWLKEGVGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKC  
YIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFQPTVVVASQVDQGANFSEVS  
NTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTSEIIRRSHLQLLNSKASL  
CVSSFFAISWALLPLSPYIMLK

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 258-281

**N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,  
220-224

**N-myristoylation sites.**

amino acids 52-58, 126-132, 188-194

## **FIGURE 61**

TGACGTCAGAATCACCAATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG  
CACCAAGGAGCCCCTCCGGGTAGCTACTACCCCTGGACCCCCAATAGTGGAGGGCAGTATGGTAGT  
GGGCTACCCCCCTGGGTGGTTATGGGGTCTGCCCTGGAGGGCCTATGGACCACAGCTGG  
TGGAGGGCCCTATGGACACCCCAATCCTGGATGTTCCCTCTGGAACCTCCAGGAGGACCATATG  
GCGGTGCAGCTCCCCGGGGCCCTATGGTCAGCCACCTCCAAGTCCCTACGGTGCCAGCAGCCT  
GGGCTTATGGACAGGGTGGGCCCTCCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC  
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA  
ATTGGTCTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTGACAAGACCAAGTCA  
GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGAAAGAACCTT  
CCAGCAGTTATGACCGGGACCGCTCGGGCTCATTAGCTACACAGAGCTGCAGCAAGCTCTGCC  
AAATGGGCTACAACTGAGCCCCAGTTCACCCAGCTTCTGGTCTCCGCTACTGCCACGCTCT  
GCCAATCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA  
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGCAACATCCGGCTCAGCTCGAGGACTCGTCA  
CCATGACAGCTTCTCGGATGCTATGACCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT  
TCCTGGCTCTTAGAGTGAGAGAAAGTATGTGGACATCTCTTTCCGTCCCTCTAGAAGAAC  
ATTCTCCCTTGCTTGATGCAACACTGTTCAAAAAGAGGGTGGAGAGTCCTGCATCATAGCCACCA  
AAATGTGAGGACCGGGCTGAGGCCACACAGATAGGGGCTGATGGAGGAGAGGATAGAAGTTGA  
ATGTCTGTATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCTTGTAATTGG  
AGTTAGTGTCCCAGTCAGCTGAGCTCCACCCCTGATGCCAGTGGTGAGAGTGTTCATCGGCCTGT  
TACCTGTGTTTAACTTCTAGCTGCCTGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGC  
ATCTTGCCAGGCTTCTGCCCCCTGCAGCTGGACCCCTCATTGCCTGCCATGCTCTGCTCGG  
CTCAGTCTCCAGGAGACAGTGGTACCTCTCCCTGCCAATACTTTTAATTGCATTTTTC  
ATTGGGGCAAAAGTCCAGTGAAATTGTAAGCTCAAAAAGGATGAAACTCTGA

## **FIGURE 62**

MASYPYRQGCPGAAGQAPGAPPGSYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG  
HPNPGMFPSTPGGPYGGAAPGGPYGQPPPSSYGAQQPGLYQGGAPPNVDPPEAYSWFQSVDSDH  
SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSAWKFIQQWKNLFQQYDR  
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQLTEAFREK  
DTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-  
66, 70-75, 78-83, 83-88, 87-92, 110-115

### **FIGURE 63**

CAGGATGCAGGGCCCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGCTGTCTTCATC  
TCCCAGGCCTTTGCCCGGAGCATCGGTGTTGGAGGAGAAAGTTCCAAAATTCGGGACC  
AACTTGCCCTCAGCTCGGACAACCTCCTCACTGGCCCCCTAACTCTGAACATCCGAGCCCCGC  
TCTGGACCCTAGGTCTAACGTGGCAAGGGTTCTGCAGTCAGAGTGGCCCTCCATCGTGGGGCTGCCTGCCATG  
GCTTCCCACCTGCAGGAGGTTCTGCAGTCAGAGTGGCCCTCCATCGTGGGGCTGCCTGCCATG  
GATTCCCTGGCCCCCTGAGGATCCTGGCAGATGATGGCTGCTGCAGGACGCCCTGGGGGA  
AGCGCTGCCTGAAGAACTCTTACCTCTCAGTGCCTGCCAGGCCCCCTCGCTCCGGGAGTGGCCCTT  
TGCCTGGGAGTCTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACCTCCACCAGGAC  
TCGGAGTCCAGACGACTGCCCGTTCTAACACTGGGAGCCGGGGAAAAATCCTTCCAAACG  
CCCTCCCTGGTCTCATCCACAGGGTTCTGCCTGATCACCCCTGGGTACCCCTGAATCCCAGTG  
TGCCTGGGAGGTTGGAGGCCCTGGACTGGTGGGAACGAGGCCATGCCACACCCTGAGGGA  
ATCTGGGTATCAATAATCAACCCCCAGGTACCACTGGGAAATATTAATCGGTATCCAGGAGG  
CAGCTGGGAAATATTAATCGGTATCCAGGAGGAGCTGGGAAATATTAATCGGTATCCAGGAG  
GCAGCTGGGAAATATTCACTATACCCAGGTATCAATAACCCATTCCCTGGAGTTCTCCGC  
CCTCCTGGCTTCTGGAACATCCCAGCTGGCTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG  
GGGTAGAGCACGATAGAGGGAAACCCAACATTGGGAGTTAGAGTCTGCTCCGCCCTTGCTG  
TGTGGGCTCAATCCAGGCCCTGTTAACATGTTCCAGCACTATCCCCACTTTCAGTGCCTCCCC  
TGCTCATCTCCAATAAAATAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

## **FIGURE 64**

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPQPAL  
DPRSNDLARVPLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPEDPWQMMAAAEDRLGEA  
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRLPRNSNLGAGGKILSQRP  
PWSLIHRVLPDHPWGTLNPSVSWGGGPCTGWGTRPMHPPEGIWGGINNQPPGTSGNINRYPGGS  
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPVGVLRPPGSSWNIPAGFPNPPSPRLQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,  
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

## **FIGURE 65**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCATCCCAGGAGCGCAGTGGCCACTATGGGTC  
TGGGCTGCCCTTGCTCCTCTTGACCCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA  
CTTGCAACTGAAGCTGAAGGAGTCTTGACAAATTCCCTCATGAGTCCAGCCTGGAA  
TTGCTTGAAAAGCTGCCTCCCTCCATCTCCCTCAGGGACCAGCGTCACCCCTCCACCATGC  
AAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCATTGAAGCCTGTGTCTTGGCCC  
GGGCTTTGGGCCGGGATGCAGGAGGCAGGCCCCGACCCGTCTTCAGCAGGGCCCCACCCTC  
CTGAGTGGCAATAATAAAATTCGGTATGCTG

## **FIGURE 66**

MGSGLPLVLLLTLGGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSGTSVTL  
HHARSQHHVVCNT

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 37-41

**N-myristoylation sites.**

amino acids 15-21, 19-25, 60-66

## **FIGURE 67**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCGGGC  
CAGGTGCCCGTCGCAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGCGAGCGCGAGAACCCCC  
TTCCTCGCGCTGCCAACCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGCTGCTTCTGGCG  
CTGGGCCTGCCGTTCTGCTGGCCGCTGGGCGAGCCTGGGGCAAATACAGACCACCTCTGC  
AAATGAGAATAGCACTGTTTGCCCTCATCCACCAGCTCCAGCTCCAGTGGCAACCTGCGTCCGG  
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTTTGGCTGCCTTGCTCCTGGCTGTGGGCTG  
GCACTGTTGGTGCAGCTTCGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCAGTAGCGA  
GGAGCAGTTCTCCCCATGCAGCCGAGGCCCGGGCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT  
GCCTGCCCATCTAGTCCCCCTCCTGCATCTGTCTCCATTGCTGTGACCTTGGGAAA  
GGCAGTGCCCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGAAGAAGGTACTCAA  
AGACTCTGCCCTGAGGTCAAGAGAGGATGGGCTATTCACTTTATATTTATATAAAATTAG  
TAGTGAGATGTAAAAAAAAAAAAAA

## **FIGURE 68**

MANPGLLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSSSSDGTLRPEAITAIIVVFS  
LLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

**Important features:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 56-80

**N-glycosylation site.**

amino acids 36-40

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 86-90

**Tyrosine kinase phosphorylation site.**

amino acids 86-94

**N-myristoylation sites.**

amino acids 7-13, 26-32

## FIGURE 69

## **FIGURE 70**

MGLFRGFVFLVLCLLHQSNSTSFIKLNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTTASTYLFE  
ATEKRFFFKNVSILIPENWKENPQYKRPKHENKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY  
IHFTPDLGGKKQNEYGPPGKLHVHEWAHLRGVFDEYNEDQPFYRAKSKKIEATRC SAGISGRN  
RVYKCQGGSCLSACRIDSTTKLYGKDCQFPDKVQTEKASIMFMQSIDS VVEFCNEKTHNQEAP  
SLQNIKCNFRSTWEVISNSEDFKNTIPMVT PPPPVFSLLKISQRIVCLVLDKGSMGGKDRLNR  
MNQAAKHFLQLQTENG SWGMVHF DSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK  
YAFQVIGELHSQDGSEVLLTDGEDNTASSCIDEVKQSGAIVHFI ALGRAADEAVIEMSKITGG  
SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGTLNSNAWMNDTVIIDSTVGKDTFFL  
ITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR  
AANSSVPPITVNAMNKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNA  
GADSFKNDGVYSRYFTAYTENGRYSLKVRAHGGANTARLKL RPPLNRAAYIPGWWVNGEIEANPP  
RPE IDEDTQTTLED FSRTASGGAFVVSQVPSLPLPDQYPPSQITDLDATVHEDKII LTWTAPGDN  
FDVGKVQRYIIRISASILDLRDSFDDALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAI  
KSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPTPTPKSHNSGVNISTLVLSIGSVVI  
VN FILSTTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

## **FIGURE 71**

CTCCCTAGGTGGAAACCTGGGAGTAGACTGACAGCAAAGACCGGGAAAGACCATACTGCCCCGGCAGGGTGA  
CAACAGGTGTCATTTGATCTCGTGTGCTGCCCTCCATTTCAGGAAAGACGCCAAGGTAAATTGACCCA  
GAGGAGCAATGATGTAGGCCACCTCCATACTTCCCTTGAAACCCAGTTATGCCAGGATTACTAGAGAGTGTCA  
ACTCAACCAAGCAAGCGGCCTTCGGCTTAACCTGTGGTGGAGGAGAACCTTGTGGGGCTCGTTCTTAGCA  
GTGCTCAAGTGAACCTGGCTGAGGGTGGACAGAAGAAAGGAAAGTCCCTCTGCTGTTGGCTGCACATCAGGA  
GGCTGTGATGGAATGAAGTGAAGGAAACTTGGAGATTCACTCAGTCATTGCTCTGCTGCAAGATCATCCTTAA  
AGTAGAGAAGCTGCTGTGGTGGTTAACTCCAAGAGGCAGAACCTGTTCTAGAAGGAAATGGATGCAAGCAGCTC  
CGGGGGCCCAAACCCATGCTCTGGTCTAGGCCAGGGAGCCCTGGGGGGCGCTTGAGGGATGCCC  
ACCGGTTCTGGACGATGGCTGAATCTGATGGTCTGCGGGGGCTGCTGGTGGATTTCGGGGTGGT  
GTTTGCTGCTGCTCTGCTGTATCTGCTGATCATGTTGGCTGCAACCCAAAAGGTGACGAGGAGCAG  
CTGGCACTGCCAGGGCAACAGCCCCAGGGAGGGTACCAAGGCCGTCCTCAGGAGTGGAGGAGCAGCAC  
CGCAACTACGTGAGCAGCCTGAAGCGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGTGAGCACCTCAGG  
AATGGGCACTAACAGCAGGGATGCTGCTGGCTGGTCTGGACAGGCCAGGGAGCCCTCAGGAGAAAACCCAGGCCACCTC  
CTGGCCTCTGCACTGGCAGGAGCAAGGAGGGTGAATGCTGGCTCAAGCTGGCCAGAGTATGCAAGCAGTG  
CCTTCGATGCTTACTCTACAGAAGGTGACCTGGAGACTGGCTTACCCGCCACCCGAGGAGAACCTG  
AGGAAGGACAAGCGGGATGAGTTGGTGAAGGCAATTGAATCAGCCTGGAGACCCGTAACAATCTGCAAGAGAACAGC  
CCCAATCACCGTCTTACACGGCTCTGATTTCATAGAAGGATCTACCGAACAGAAAGGACAAGGGACATTGTAT  
GAGCTCACCTTCAAAGGGCACACACAGAATTCAAGGCTCATCTTATTCGACCAATTCAACCCCATCATGAAA  
GTGAAAAATCAAAGGCTAACATGGCCAACACGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGGACAAGTTC  
CGGCAGTTCATGCAAGATTCAAGGGAGATGTCATTGAGCAGGATGGAGACTTCATCTCACTGTTTACTTGG  
AAAGAAGAATAATGAAGTCAAAGGAATACTGAAAACACTTCAAAGCTGCCAACTTCAGGAATTTCATC  
CAGCTGAATGGAGAATTCTCGGGGAAAGGGACTTGTGTTGGAGCCGCTCTGGAAAGGAAAGCAACGCTTCTC  
TTTTCTGCTGATGTCAGTACTTACATCTGAATTCTCAATACGTTGAGGCTGAATACACAGCCAGGGAAAGAAG  
GTATTTTATCCAGTTCTTCACTGCTGATACAATCCGGATAATATAACGGCCACCATGATGCACTCCCTCCCTGG  
CAGCAGCTCATGCAAAAGGAAACTGGATTGGAGAGACTTGGATTGGGATGACCTGTCAGTATCGTCAGAC  
TTCATCAATAGTGGTTGATCTGGACATCAAAGGCTGGGGGGAGAGGATGTCACCTTATCGCAAGTATCTC  
CACAGCAACCTCATAGTGGTACGGACGCCGTGCGAGGACTCTCCACCTCTGGCATGAGAACGCTGCATGGACGAG  
CTGACCCCCGAGCACTACAAGATGTCATGCACTCCAAAGGCAATGACAGGAGCATCCACGGCCAGCTGGGATGCTG  
GTGTTCAAGGAGCAGGATAGAGGCTCACCTCGAAACAGAAAGAGACAAGTAGCAGGAAACATGAACCTCCAGA  
GAAGGATTGGGAGACACTTTCTTTCGCAATTACTGAAAGTGGCTGCAACAGAGAAAAGACTCCATAAA  
GGACGACAAAAGAATTGGACTGATGGTCAAGAGATGAGAAAGCCTCGATTCTCTGTTGGGTTTACAACAGA  
AATCAAATCTCCGTTGCTGCAAAGTAACCCAGTTGACCCCTGTGAAGTGTGACAAAGGAGAACATGCTGT  
AGATTATAAGCCTAATGGTGGAGGTTTGATGGTTTACAATACACTGAGACCTGTTGTTGCTCATG  
AATATTCTGATGTTAAAGAGCAGTTGAAAGGAAATTCTAGGATGAAAGGCAAGCATATTCTCTCATATGATG  
GCCTATCAGCAGGGCTCTAGTTCTAGGAATGCTAAATATCAGAAGGAGGAGGAGATAGGCTTATTATGATG  
AGTGAAGTACATTAAGTAAAATAATGGACCAGAAAAGAAAAGAACATAATATCGTCATATTCCCCAAGAT  
TAACCAAAAATCTGTTATCTTGGTTGTCCTTTAACTGTCCTGTTTCTTATTTAAAATGCACT  
TTTTCTGCTTGTGACTTATGCTGTTATTTAATACCAACTTCTGCAAGCTTACAAGAGAGACAAGTGGCTAC  
ATTTTATATTCTGAGGAAAGGAAACTTGTGAGGATGCTTATGAGAAACTTCTGCTTCAAGGATCAATTGATGCCATAT  
CCAAGGACATGCCAATGCTGTTCTGAGGACTGAATGTCAGGCAATTGAGACATAGGGAGGAAATGGTTGACT  
AATACAGACGATACAGATACTTCTGCAAGAGTATTGCAAGAGGAGCAACTGAAACACTGGAGGAAAAGAAAATGAC  
ACTTCTGCTTACAGAAAAGGAAACTCATTGAGCTGGTATCTGATGTCACCTAAAGTCAGAACCCACATT  
CTCCTCAGAAGTAGGGACCGCTTCTACCTGTTAAATAACCAAGTACCGTGTGAACCAAAACATCTTTT  
AAAACAGGGTGTCTCTGGCTTCTGGCTTCCATAAGAAGAAAATGGAGAAAATATATATATATATATATTGT  
GAAAGATCAATCCATGCCAATCTGAGGATGGAAGTTTGCTACATGTTATCCACCCAGGGCAGGTGGAAG  
TAAGTGAATTATTTTAAATTAAAGCAGTTCTACTCAATCACCAAGATGCTCTGAAAATTGCAATTAC  
CAAACATTGTTAAATAACAGTTAACATAGAGTGGTTCTCATTGATGAAAATTATTAGCCAGCAC  
ATGCAAGCTGTTGGTGTGTTAAAAATGCAATTGATTTGACTGGTAGTTGAAATTAAATTAAACACAGG  
CCATGAATGGAAGGTGGTATTGCAAGCTAATAATTATGATTTGTTGAA

## **FIGURE 72**

MMMVRRGLLAWISRVVVLVLLCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWE  
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK  
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVRKDKRDELVEAIESALETLNNPA  
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVNEKLMAN  
TLINIVPLAKRVDKFRQFMQNFRREMTCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF  
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFQSQY  
NPGIIYGHHDAVPPLQQQLVIKETGFWRDFGFGMTQCYSDFINIGGFDL DIKGWGGEDVHLYR  
KYLHSNLIVV RTPVRGLFHLWHEKRCMDEL TPEQYKCMQSKAMNEASHGQLGMLVFRHEIEAHL  
RKQKQKTSSKKT

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 315-319, 324-328

**N-myristoylation sites.**

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

**Amidation site.**

amino acids 377-381

## **FIGURE 73**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGAGTTGCTCTGGGATCCA  
GAAACCCATGATAACCCTACTGAACACCGAATCCCCTGGAAGGCCACAGAGACAGAGACAGCAAGA  
GAAGCAGAGATAAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCACTCCTC  
CCTCCCTCTCTCGCTGTCTAGTCCTCTAGTCCTCAAATTCCAGTCCCTGCACCCCTTC  
CTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTGGATCCTGGCTGCAGATGGG  
GTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATGGCCAGCCTTACCTGAGTGT  
GGAAACAATGCCAGTCGCCATCGATATTGACAGACAGCAGTGTGACATTGACCTGATTGCC  
TGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTGGACCTGCACAACAATGCC  
ACACAGTGCAACTCTCTGCCCTACCCGTATCTGGTGGACTCCCCGAAAATATGTAGCT  
GCCAGCTCCACCTGCACTGGGTGAGAAAGGATCCCCAGGGGGTCAAGAACACCAGATCAACAG  
TGAAGCCACATTGAGAGCTCACATTGTACATTATGACTCTGATTCTATGACAGCTGAGTG  
AGGCTGCTGAGAGGCCCTCAGGGCCTGGCTGTCCTGGCATCCTAATTGAGGTGGTGGACTAAG  
AATATAGCTTATGAAACACATTCTGAGTCACCTGCATGAAGTCAGGCATAAAGATCAGAAGACCTC  
AGTGCCTCCCTTAACCTAACAGAGAGCTGCTCCCCAACAGCTGGGAGTACTCCGCTACAATG  
GCTCGCTCACAACTCCCCCTGCTACCAGAGTGTGCTGGACAGTTTTATAGAAGGTCCAG  
ATTTCATGAAACAGCTGGAAAAGCTTCAGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAA  
GCTTCTGGTACAGAACTACCGAGCCCTCAGCCTCTCAATCAGCGCATGGCTTGCTTCA  
TCCAAGCAGGATCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGAGGAATCTGGTTGGC  
TGTCTGCTTCTCCTGGCTGTTATTCATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAA  
CCGAAAGAGTGTGGCTTCACCTCAGCACAAGCCACGACTGAGGCATAAATTCCCTCAGATAC  
CATGGATGTGGATGACTTCCCTCATGCCTATCAGGAAGCCTCTAAATGGGTGAGGATCTGG  
CCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCCTGGACATCTTAGAGAGGAAT  
GGACCCAGGCTGTCATTCCAGGAAGAAGCTGCAGAGCCTCAGCCTCTCCAAACATGTAGGAGGAA  
ATGAGGAAATCGCTGTTGTTAATGCAGAGANCAAACCTGTTAGTGCAGGGGAAGTTGGG  
ATATACCCAAAGTCCCTACCCCTCACTTTATGCCCTTCCCTAGATATACTGCAGGATCT  
CTCCTAGGATAAAAGAGTTGCTGTTGAAGTGTATATTGATCAATATATTGAAATTAAAG  
TTCTGACTTT

## **FIGURE 74**

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSTFDPLPALQ  
PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEAT  
FAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP  
FNLRELLPKQLGQYFRYNGSLTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV  
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS  
VVFTSAQATTEA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## **FIGURE 75**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCCCTGGGACGGCAGTCCCTGTGTC  
TCTGGTGGTTGCCTAACCTGCAAACATCACCTTATCCATCAACATGAAGAATGTCCTACA  
ATGGACTCCACCAGAGGTCTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTCATCACAA  
ATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGCTGACAGCTCC  
AGAGAAGTGAAGAGAAATCCAGAAGACCTCCTGTTCCATGCAACAAATATACTCCAATCTGA  
AGTATAACGTGCTGTGTTGAATACTAAACAGAACGTGGTCCAGTGTGACCAACCAC  
ACGCTGGTGCACCTGGCTGGAGCCGAACACTCTTACTGCGTACACGTGGAGTCCTCGTCCC  
AGGGCCCCCTCGCCGTGCTCAGCCTCTGAGAAGCAGTGTGCCAGGACTTGAAAGATCAATCAT  
CAGAGTCAAGGCTAAAATCATCTCTGGTATGTTGCCATATCTATTACCGTGTCTTT  
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGCAAAGAGAAACACCCAGCAAATTT  
GATTTGATTATGAAATGAATTGACAAAAGATTCTTGTGCCTGCTGAAAAAAATCGTGATTA  
ACTTTATCACCCCTCAATATCTCGGATGATTCTAAATTCTCATCAGGATATGAGTTACTGGGA  
AAAAGCAGTGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA  
GGAAGAGGAGGTGAAACATTAGGGTATGCTTCGCAATTGATGAAATTGGACTCTGAAG  
AAAACACCGAAGGTACTTCTCACCCAGCAAGAGTCCCTCAGCAGAACAAACACCCCCGGATAAA  
ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTGCGGGGCCTGAAGAGCAGGA  
GCTCAGTTGCAGGAGGAGGTGTCACACAAGGAACATTGGAGTCGCAGGCAGCGTGGCAG  
TCTTGGGCCGCAAACGTTACAGTACTCATACACCCCTCAGCTCCAGACTTAGACCCCTGGCG  
CAGGAGCACACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCCTGGTCACTGGGA  
TCCCCAAACTGGCAGGCTGTGATTCCCTCGCTGTCAGCTCGACCAAGGATTAGAGGCTGCG  
AGCCTCTGAGGGGGATGGCTGGAGAGGAGGGCTTCTATCTAGACTCTATGAGGAGCCGCT  
CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTGAGGAATGGGGTTATA  
TGTGCAGATGGAAAACTGGCCAACACTTCCTTTGCCTTGTGAAACAAGTGA  
TCACCCCTTGATCCCAGCCATAAAAGTACCTGGATGAAAGAAGTTTCCAGTTGTCAGTGT  
CTGTGAGAATTACTTATTCTTCTATTCTCATAGCACGTGTGATTGGTTCATGCATGTA  
GGTCTCTAACATGATGGTGGCCTCTGGAGTCCAGGGGCTGGCCGGTTGTTCTATGCAGAGAA  
AGCAGTCAATAATGTTGCCAGACTGGGTGCAGAATTATTCAAGGTGGGTGT

## **FIGURE 76**

MSYNGLHQRFKELKLLTLCISISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY  
SNLKYNVSLNTKSNRTWSQCVTNHTLVLWLEPNLTYCVHVESFVPGPPRRAQPSEKQCARTLK  
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGYNEFDKRFFVPAEK  
IVINFITLNISDDSKISHQDMILLGKSSDVSSLNDPQPSGNLRPPQEEEVKHLGYASHLMEIFC  
DSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQELSLQEEVSTQGTLESQA  
ALAVLGQPQLQYSYTPQLQDLDPLAQEHTDSEEGPEEPSTTLVDWDWPQTGRLCIPSLSSFDQDS  
EGCEPSEGDSLGEGLSRLYEEPAPDRPPGENETYLMQFMEEWGLYVQMN

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

## **FIGURE 77**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCAC TTGCTGCCCTTGACAC  
CTGGGAAGATGGCGGGCCGTGGACCTTCACCCCTCTCTGTGGTTGCTGGCAGCCACCTTGATC  
CAAGCCACCCCTCAGTCCCCTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC  
ACAGGGAGCTGAAGGACCACAACGCCACCAGCATTGCAGCTGCCCTGCTCAGTGCCATGC  
GGGAAAAGCCAGCGGGAGGCATCCCTGTGCTGGCAGCCTGGTGAACACCGTCTGAAGCACATC  
ATCTGGCTGAAGGTCACTCACAGCTAACATCCTCCAGTCAGGTGAAGCCCTGGCCAATGACCA  
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAAGACCA  
TCGTGGAGTTCCACATGACGACTGAGGCCAAGGCCACCATCCGCATGGACACCAGTGAAGTGGC  
CCCACCCGCCTGGTCTCAGTGA C TGTGCCACCAGCCATGGAGCCTGCGCATCCA ACTGCTGTA  
TAAGCTCCTCCCTGGTGAACGCCCTAGCTAACAGCAGGTCAAGCAGGCTCATGGACCTCC  
CCAATCTAGTGA AAA ACCAGCTGTGCTCCCGT GATCGAGGCTTCAATGGCATGTATGCAGAC  
CTCCTGCAGCTGGTGAAGGTGCCCTTCCCTCAGCATTGACCGTCTGGAGTTGACCTCTGTA  
TCCTGCCATCAAGGGT GACACCATT CAGCTCACCTGGGGCCAAGTTGTTGGACTCACAGGGAA  
AGGTGACCAAGTGGTCAATAACTCTGCAGCTCCCTGACAATGCCACCCCTGGACAACATCCCG  
TTCAGCCTCATCGTAGTCAAGGACGTGGTGAAGAGCTGCAGTGGCTGCTGTGCTCTCCAGAAGA  
ATTCAATGGTCTGTGGACTCTGTGCTTCCTGAGAGTGCCCATGGCTGAAGTCAAGCATGGGC  
TGATCAATGAAAAGGCTGCAGATAAGCTGGATCTACCCAGATCGTGAAGATCTTAACACTCAGGAC  
ACTCCCGAGTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGTGGAGTT  
TCCCTCCAGTGAAGCCCTCCGCCCTTGTCAACCTGGCATCGAACGCCAGCTCGGAAGCTCAGT  
TTTACACCAAAGGTGACCAACTTAACTCAACTTGAATAACATCAGCTCTGATGGATCCAGCTG  
ATGAACCTCTGGGATTGGCTGGTCCAACCTGATGTTGAAAAACATCATCACTGAGATCATCCA  
CTCCATCCTGCTGCCGAACCAGAAATGGCAAATTAAAGATCTGGGTCCCAGTGTCAATTGGTGAAGG  
CCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTGTGCTTACTCCAGCCTCC  
TTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTGGATGGCAGCCATCAGGGAAAGGCTGG  
GTCCCAAGCTGGAGTATGGGTGTGAGCTATAGACCATCCCTCTGCAATCAATAAACACTTG  
CCTGTGAAAAA

## **FIGURE 78**

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPVKIKEKLTQELKDHNATSILQQPLLSAMREK  
PAGGIPLVGLSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE  
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL  
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKLDSQGKVT  
KWFNNSAASLTMPTLDNIPFSLIVSQDVVKAAAVAVLSPEEFMVLLDSVLPESAHLRKSSIGLIN  
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEALRPLFTLGIEASSEAQFYT  
KGDQLILNLNNISSLRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSLVKALG  
FEAAESSLTKDALVLTPASLWKPSSPVSQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

## **FIGURE 79**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC  
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTCTACTGAGAGGTCTGCCATGGCCTCT  
CTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGCTTGGGACACTGGTGCCAT  
GCTGCTCCCCAGCTGGAAAACAAGTTCTATGCGGTGCCAGCATTGTGACAGCAGTGGCTCT  
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC  
ACCCTCTGGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGATGGTGACATCCAGTGCAAT  
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGCATGAGATGCACAGTCTCTGCCAGGAATCCC  
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTATCCTTGAGGCCCTGGGATTC  
ATTCCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTCACCACCTGGTGCTGACAG  
CATGAAATTGAGATTGGAGAGGCTCTTACTGGGCATTATTCTCCCTGTTCTCCCTGATAG  
CTGGAATCATCCTCTGCTTTCTGCTCATCCAGAGAAATCGCTCCAACACTACGATGCCAAC  
CAAGCCCAACCTCTGCCACAAGGAGCTCCAAGGCCTGGTCAACCTCCAAAGTCAAGAGTGA  
GTTCAATTCTACAGCCTGACAGGTATGTGTGAAGAACCAGGGCCAGAGCTGGGGGTGGCTG  
GGTCTGTGAAAAACAGTGGACAGCACCCGAGGGCCACAGGTGAGGGACACTACCAACTGGATCGT  
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGCCATTGGATTGACCAAAGGCAGAAATGGGG  
GCTAGTGTAACAGCATGCAGGTTGAATTGCAAGGATGCTGCCATGCCAGCCTTCTGTTTCC  
TCACCTGCTGCTCCCTGCCCTAAGTCCCCAACCTCAACTGAAACCCATTCCCTTAAGCCA  
GGACTCAGAGGATCCCTTGCCCTCTGGTTACCTGGACTCCATCCCCAACCCACTAATCACA  
TCCCACGTGACTGACCCCTCTGTGATCAAAGACCCCTCTCTGGCTGAGGTTGGCTCTAGCTCATT  
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTGTGGCATTGCTCTAACCTACTTCTCAAGCTTC  
CCTCCAAAGAAACTGATTGCCCTGGAACCTCCATCCACTCTGTATGACTCCACAGTGTCCA  
GACTAATTGTGCACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG  
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTAAAAAAATA

## **FIGURE 8o**

MASLGLQLVGYILGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD  
IYSTLLGLPADIQAAQAMMVTSIASSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL  
LGFIPVAWNLHGLRLDFYSPLVPSMKFEIGEALYLGISSLFSLIAGIILCFSCSSQRNRSNYY  
DAYQAQPLATRSSPRPGQPPKVSEFNSYSLTGYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

## **FIGURE 81**

CCACACCGTCCGCCCTCCTCCCTCTGGACCTTCCTCGTCTCCATCTCTCCCTCTTC  
CCCGCGTTCTTTCCACCTTCTTCTTCCACCTTAGACCTCCCTGCCCTCTTCCT  
GCCCACCGCTGCTTCCCTGGCCCTCTCCGACCCCGCTCTAGCAGCAGACCTCCCTGGGTCTGTGG  
GTTGATCTGTGGCCCTGTGCCCTCCGTGTCTTCTCCCTCCGACTCCGCTCCGG  
ACCAGCGGCCTGACCCCTGGGGAAAGGATGGTCCCGAGGGTGGAGGGTCTCTCCCTGCTGGGA  
CTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCGCCAGACATGTTCTGCCTTT  
CCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACTTGAGGCCACAAGGCTGATGT  
ACTGCCCTGCGCTGTACCTGCTCAGAGGGGCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT  
GTCCACTGCCCTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC  
TCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCCAGCACAACGGGACCATGTACCAACACGGAG  
AGATCTTCAGTGCCCATGAGCTGTTCCCTCCGCCCTGCCAACCAAGTGTGTCCCTGCAAGCTGC  
ACAGAGGGCCAGATCTACTGCGGCCTCACAAACCTGCCCGAACAGGCTGCCAGCACCCCTCCC  
ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGAAGTGAAGCAATGGATGAAGAGGACA  
GTGTGCAGTCGCTCCATGGGGTGGAGACATCCTCAGGATCCATGTTCCAGTGTGTGGAGAAAG  
AGAGGCCCGGGCACCCAGCCCCACTGGCCTCAGGCCCTCTGAGCTTACCCCTGCCACTT  
CAGACCCAAGGGAGCAGGCAGCACAACGTCAAGATGTCCTGAAGGAGAAACATAAGAAAGCCT  
GTGTGCATGGCGGGAAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCTTCCGTGCCTCGC  
CCCTTGCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC  
CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCAGAGG  
ACAAAGCAGACCCCTGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCGGGTC  
CTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTGCCTGGAACACGAGGC  
CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAAACTGAGGCTCAGAGAG  
GTGAAGTACCTGGCCAAGGCCACACAGCCAGAACTTCCACTTGACTCAGATCAAGAAAGTCAG  
GAAGCAAGACTTCCAGAAAGAGGCACAGCACTCCGACTGCTCGCTGGCCCCACGAAGGTCACT  
GGAACGTCTTCCCTAGCCCAGACCCCTGGAGCTGAAGGTACGGCAGTCCAGACAAAGTACCAAG  
ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAA  
TAAGAAGTTGCATTACCCCTCAAAAAAAAAAAAAAA

## **FIGURE 82**

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE  
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELP  
PSRLPNQCVLCSCTEGQIYCGLTTCPPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR  
HQDPCSSDAGRKRGPGBTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKKKACVHGGKTYS  
HGEVWHPAFRAFGPLCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKCKKICCPEDKADPGHSE  
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH  
SQNLPLSDQESQEARNPERGTALPTARWPPRRSLERLPSPDPGAEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

## **FIGURE 83**

GACAGCTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCCGCTCACGCAGAGCCTCTCC  
GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTCTAATCCATCCGTACCTCTCCTGTCA  
TCCGTTCCATGCCGTGAGGTCCATTACAGAACACATCCTGGCTCTCATGCTCAGTTGGTCTGAGTC  
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTGGGCCAGACAAGCCTGTCCAGGCCTGGTGGGGAG  
GACGCAGCATTCTCTGTTCTGCTCTAAGACCAATGCAGAGGCCATGGAAGTGCAGTTCTCAGGGG  
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCATTATGCAGATGCCACAGTATC  
AAGGCAGGACAAAATGGTGAAGGATTCTATTGCGGAGGGGCGATCTCTGAGGCTGGAAAACATTACT  
GTGTTGGATGCTGCCCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAACGGCATCTGGAGCT  
ACAGGTGTCAGCACTGGCTCAGTTCTCTCATTTCCATCACGGATATGTTGATAGAGACATCCAGCTAC  
TCTGTCAGTCCTCGGGCTGGTCCCCGGCCACAGCGAAGTGGAAAGGTCACAAGGACAGGATTGTCC  
ACAGACTCCAGGACAAACAGAGACATGCATGCCGTGTTGATGTGGAGATCTCTGACCGTCCAAGAGAA  
CCCGGGAGCATATCCTGTTCCATGCCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG  
GAGATACCTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGAATACTCTGCTGTGGCCTA  
TTTTTGGCATTGTTGACTGAAGATTTCTCCTCCAAATTCCAGTGGAAATCCAGGCCAACTGGACTG  
GAGAAGAACGACGGACAGGCAGAATTGAGAGACGCCGAAACACGCAGTGGAGGTGACTCTGGATCCAG  
AGACGGCTCACCCGAAGCTCTGCCGTTCTGATCTGAAACTGTAACCCATAGAAAAGCTCCCAGGAGGTG  
CCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGCTCTCAGAGTTCCAAGCAGGGAAACATTA  
CTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGCTGGAGTGTGCCGGATGATGTGGACAGGAGGA  
AGGAGTACGTGACTTTGCTCCGATCATGGTACTGGGTCTCAGACTGAATGGAGAACATTGTATTTC  
ACATTAATCCCGTTTATCAGCGTCTCCCCAGGACCCCACCTACAAAAAATAGGGTCTCCTGGACTA  
TGAGTGTGGACCATCTCTTCTTCACATAAATGACCAGTCCCTTATTATACCCCTGACATGTCGGTTG  
AAGGCTTATTGAGGCCCTACATTGAGTATCCGCTCTAATGAGAAAATGAAACTCCATAGTCATG  
CCAGTCACCCAGGAATCAGAGAAAAGAGGCCCTCTGGCAAAGGCCCTCTGCAATCCCAGAGACAAGCAACAG  
TGAGTCCTCCTCACAGGCAACCACGCCCTCTCCCCAGGGTGAATGTAGGATGAATCACATCCCACAT  
TCTCTTTAGGGATATTAAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCGGCCAAGGTGGCTTCCA  
GATGAAGGGGACTGCCGTGTCACATGGGAGTCAGGTGTCAGGCTGCCCTGAGCTGGAGGGAAAGAAGG  
CTGACATTACATTAGTTGCTCTCACTCCATCTGGCTAAGTGAATCTGAATACCACCTCTCAGGTGAAG  
AACCGTCAGGAATTCCCATCTCACAGGCTGTGGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG  
ATCTTATTGATGACAGAGTGTATCCTAATGGTTGTTCAATTACACTTCACTGTTAGAAAAAA

## **FIGURE 84**

MAALMLSIVLSSLKLGSQWQVFGPDKPVQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSSVVH  
LYRDGKDQPFMOMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQKAIWELO  
VSALGSVPLISITGYVDRDIQLCQSSGWPRPTAKWKGPGQGDLSTDRTNRDMHGLFDVEISL  
TVQENAGSISCSMRRAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK  
FQWKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAPQEVPHSEKRF  
TRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLSPDHGYWVRLNGEHLYFT  
LNPRFISVFPPPTKIGVFLDYECGTISFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT  
PIVICPVTQESEKEASWQRASAIPETSNSESSSQATTPFLPRGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

## **FIGURE 85**

AACAGACGTTCCCTCGGGCCCTGGCACCTAACCCCAGACATGCTGCTGCTGCTGCCCT  
GCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTTCCGTGA  
CGGTGCAGGAAGGCCTGTGTGCCATGTGCCCTGCTCCTCTCCTACCCCTCGCATGGCTGGATT  
TACCCCTGGCCCAAGTAGTCATGGCTACTGGTCCGGGAAGGGGCCAATACAGACCAGGATGCTCC  
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTCCTTG  
GGGACCCACATACCAAGAATTGCACCCCTGAGCATCAGAGATGCCAGAAGAAGTGTGCGGGGAGA  
TACTTCTTCGTATGGAGAAAGGAAGTATAAAATGAAATTATAAACATCACC GGCTCTGTGAA  
TGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCAGGCACCCCTGGAGTCGGCTGCC  
AGAATCTGACCTGCTCTGTGCCCTGGCCTGTGAGCAGGGACACCCCTATGATCTCCTGGATA  
GGGACCTCCGTGTCCCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCCCTATCCCACA  
GCCCCAGGACCATGGCACCAGCCTCACCTGTCAGGTGACCTTCCCTGGGCCAGCGTGACCA  
ACAAGACCGTCCATCTCAACGTGCTCACCGCCTCAGAACATTGACCATGACTGTCTCCAAGGA  
GACGGCACAGTATCCACAGTCTGGAAATGGCTCATCTGTCACTCCCAGAGGGCAGTCT  
GCGCCTGGTCTGTGCAAGTTGATGCACTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGA  
GAGGCTGACCCCTGTGCCCTCACAGCCCTAAACCCGGGGTGCTGGAGCTGCCCTGGGTGCAC  
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCCCTCGGCTCTCAGCAGGTCTACCT  
GAACGTCCTCCCTGCAGAGCAAAGCCACATCAGGAGTGA  
CTCAGGGGGTGGTCGGGGAGCTGGAG  
CCACAGCCCTGGTCTTCCCTGTCCTCTGCGTCATCTCGTTGAGGTCTGCAGGAAGAAA  
TCGGCAAGGCCAGCAGCGGGCGTGGGAGATACGGG  
CATAGAGGATGCAAACGCTGTCAAGGGTT  
AGCCTCTCAGGGGCCCTGACTGAACCTGGCAGAAGACAGTCCCCAGACCAGCCTCCCCAG  
CTTCTGCCGCTCTCAGTGGGAAAGGAGAGCTCAGTATGCATCCCTCAGCTCCAGATGGT  
AAGCCTTGGACTCGCGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG  
ATGAGAAACTGCAGAGACTCACCTGATTGAGGATCACAGCCCTCCAGGCAAGGGAGAAGTCA  
GAGGCTGATTCTGTAGAATTAAACAGCCCTAACGTGAGCTATGATAACACTATGAATTATG  
TGCAGAGTGAAGAACACAGGCTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCC  
TCCCTTTATTTTTAACTAAAAGACAGACAAATTCCA

## **FIGURE 86**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPFSYPSHGWIYPGPVVHGYWFREG  
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLISRARRSDAGRYFFRMKEGSIKWNY  
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSVPWACEQGTPPMISWIGTSVSPLDPSTTRS  
SVLTLIPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLMTVFQGDGTVSTVLNGSSL  
SLPEGQSLRLVCAVDADSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP  
LGSQQVYLNVSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDTGIE  
DANAVRGSAQGPLTEPWAEDSPPDQPPPASARSSVGEHELQYASLSFQMVKPWDSRGQEATDTE  
YSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

## **FIGURE 87**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGGAGCTCTGTAC  
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAAATGAACCAACTCAGCTTCCTGCTGTTTC  
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT  
TCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCTAGTCATTGA  
TGGCCTGTATTTCTCCGCAGTGAGAATGGTGTATCTACCAGACCTCTGTGACATGACCTCTG  
GGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGAGTGCACGGT  
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGACGGCAACTGGC  
CAACTACAACACCTTGGATCTGAGAGGCGGCCAGAGCGATGACTACAAGAACCTGGCTACT  
ACGACATCCAGGCCAAGGACCTGGCATCTGGCACGTGCCAATAAGTCCCCATGCAGCACTGG  
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTCCTCCAGACACTGGGACATAATCT  
GTTTGGCATCTACCAGAAATATCCAGTGAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC  
CGGTGATCCCTGTGGTCTATGATTTGGCAGCAGCCCAGAAAACAGCATCTTATTACTCACCTAT  
GGCCAGCGGAATTCACTGCGGATTGTTCAAGTTCAGGTATTAATAACGAGAGAGCAGCCAA  
CGCCTTGTGCTGGAATGAGGGTACCGGATGTAACACTGAGCATCACTGCATTGGAGGAG  
GATACTTCCAGAGGCCAGTCCCAGCAGTGTGGAGATTTCTGGTTGATTGGAGTGGATAT  
GGAACTCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG  
**TTGAGAGTTTGTGGAGGGAACCCAGACCTCTCCACCACATGAGATCCAAAGGATGGAGAA**  
CAACTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGA  
AAAAAA

## **FIGURE 88**

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI  
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRSSQQGSKADYPEGDGNWANYNTFGSAAAT  
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLRYRTDTGFLQTLGHNLFGIYQKYPVKYG  
EGKCWTNDGPVIPVYDFGDAQKTASYYSPYQREFTAGFVQFRVFNNERAANALCAGMRVTGCN  
TEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSEITEAAVLLFYR

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation site.**

amino acids 163-167

**Glycosaminoglycan attachment sites.**

amino acids 74-78, 289-293

**N-myristoylation sites.**

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

## **FIGURE 89**

CTAGATTGTCGGCTTGC~~GGGG~~GACTTCAGGAGTCGCTGTCTGAAC~~TCCAGCCTCAGAGAC~~  
CGCCGCCCTTGTC~~CCC~~GAGGCCATGGGCCGGTCTCAGGGCTTGTGCCCTCGCTTCTGACG  
CTCCTGGCGCATCTGGTGGTCGTCACCTTATTCTGGTCCCGGACAGCAACATACAGGCCGT  
CCTGCCCTCACGTCACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGGTGGCCCGCGTCT  
CTGTCACCCTGGGCCTTTGCAGTGGAGCTGGCCGGTTCCTCTCAGGAGTCTCCATGTTAAC  
AGCACCCAGAGCCTCATCTCCATTGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCCTTCA  
ATTCGAGCGTTGGGAGTGCACTACGTATTGGTACATTTGTCTTCGCAGTGCCCCTCCAGCTG  
TCACTGAAATGGCTTATTCGTACCGTCTTGGCGTGAAAAAGAAACCCTTCTGATTACCTCA  
TGACGGAACCTAAGGACGAAGCCTACAGGGCAAGGGCGCTTCGTATTCCGTGAAGAAGGAAG  
GCATAGGCTTCGGTTTCCCCTCGGAAACTGCTCTGCTGGAGGATATGTTGAATAATTACG  
TCTTGAGTCTGGATTATCCGATTGTATTAGTGCTTGTAATAAAATGTTTAGTAACA  
TTAAGACTTATACAGTTTAGGGACAATTAAAAAAAAAAA

## **FIGURE 90**

MGRVSGLVPSRFLTLAHLVVVITLFWSRDSNIQACLPLTPEEYDKQDIQLVAALSVTLGLFA  
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVTEMALFV  
TVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

## **FIGURE 91**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGGAGGAAGATGCAACTGAC  
TCGCTGCTGCTCGTGTTCCTGGTGAGGGTAGCCTATCTGGTCATCTGTGCCAGGATGATG  
GTCCTCCGGCTCAGAGGACCCGTAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT  
CGGAAGGGGGCCACATCTCACCTAACGTCACAGTCCCAGGGCATGGCAATTCCACTCTCCTAGGGCTGCT  
GGCCCCGCCCTGGGGAGGCTTGGGCATTCTGGGCAGCCCCCAACGCCGAACCACAGCCCC  
CACCCCTAGCCAAGGTGAAGAAAATCTTGGCTGGGCAGTTCTACTCCAACATCAAGACGGTG  
GCCCTGAACCTGCTCGTCACAGGGAAAGATTGTGGACCATGGCAATGGACCTTCAGCGTCCACTT  
CCAACACAATGCCACAGGCCAGGGAAACATCTCATCAGCCTCGTGCCTCCAGTAAAGCTGTAG  
AGTTCCACCAGGAACAGCAGATCTCATCGAAGCCAAGGCCTCCAAAATCTCAACTGCCGGATG  
GAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTCGTTGCACCCACGCCAGCCAAGATCTG  
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTCAAAGTCGTGTG  
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAACATAC  
CATAGTGATAACCCCTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGGC  
TGGAAGGACAGGCCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAAGGGTTGGCCTC  
AGGCAGGGAGGGGGTGGAGACGAGGAGATGCCAAGTGGGCCAGGGCAAGTCTCAAGTGGCAG  
AGAAAGGGTCCAAGTGTGGTCCAAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG  
AGGAGGAGTGGCTCTGTGCAGCCTCACAGGGCTTGCACGGGAGCCACAGAGAGATGCTGG  
TCCCCGAGGCCCTGGGCAGGCCGATCAGTGTGGCCCAGATCAAGTCATGGAGGAAGCTAAGC  
CCTGGTTCTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGAGATTTCATCAGTGTGGACA  
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGTGG  
GCCAGAGGAGCTCCAGCCCTGCCCTAGTGGCGCCCTGAGCCCTGTGCTGAGCATGG  
CATGAGGCTGAAGTGGCAACCCCTGGGTCTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC  
CAGGCCACCCCTTCCAAAATCCCTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG  
GCACACCCATCCTTAAGCTAACGACAGGACGATTGTGGCTCCACACTAACGGCCACAGCCCATC  
CGCGTGTGTGTGTCCTCTGCCACCCCTGCTGGCTCTGGAGCATCCATGTCCCG  
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTAGACCCGGGTTCTCCGGATCTGGATGGC  
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGCCGGCAGAGCATGTGCTGGATCTGTT  
TGTGTGTCTGTGTGGGTGGGGAGGGGAGGGAAAGTCTGTGAAACCGCTGATTGCTGACTTT  
TGTGTGAAGAATCGTGTCTGGAGCAGGAATAAGCTTGCCCCGGGCA

## **FIGURE 92**

MQLTRCCFVFLVQGSILYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL  
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNNGTF  
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDP  
AKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKCPDNYHSDTPYYPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

### **FIGURE 93**

CGGTGGCC**A**TGACTGCGGCCGTGTTCTCGGCTGCGCCTTCATTGCCTCGGGCTGCGCTGCC  
CTTTATGTCTTACCATGCCATCGAGCCGTTGCGTATCATCTTCCTCATGCCGGAGCTTCTT  
CTGGTTGGTGTCTACTGATTGCTCCCTGTTGGTTCATGGCAAGAGTCATTATTGACAACA  
AAGATGGACCAACACAGAAATATCTGCTGATCTTGGAGCGTTGCTCTGTCTATATCCAAGAA  
ATGTTCCGATTGCATATTATAAAACTCTTAAAAAAAGCCAGTGAAGGTTGAAGAGTATAAACCC  
AGGTGAGACAGCACCCCTATGCGACTGCTGGCTATGTTCTGGCTGGCTTGGATCATGA  
GTGGAGTATTTCCCTTGTAATACCCATCTGACTCCTGGGCCAGGCACAGTGGCATTCA  
GGAGATTCTCCTCAATTCTCCTTATTCACTGGCTGACGCTGGCATTATCTTGCTGCATGT  
ATTCTGGGCATTGTATTTGATGGCTGTGAGAAGAAAAGTGGGCATCCTCCTATCGTC  
TCCTGACCCACCTGCTGGTGTCAAGCCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG  
TCAGCATTATAATCCTGGTGCTCATGGCACCTGGCATTCTAGCTGCGGGAGGCAGCTGCCG  
AAGCCTGAAACTCTGCCTGCTCGCCAAGACAAGAACCTTCTTACAACCAGCGCTCCAGAT  
**AACCTCAGGGAACCAGCACTCCCCAACCGCAGACTACATCTTAGAGGAAGCACAACGTGCCT**  
TTTCTGAAAATCCCTTTCTGGTGGATTGAGAAAGAAATAAAACTATGCAGATA

## **FIGURE 94**

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG  
PTQKYLLIFGAFVSVIQEMFRFAYYKLLKASEGLKSINPGETAPSMRLLAYVSGLGFMSGV  
FSFVNNTLSDSLGP GTVG I HGDSPQFFLYSAFMTLVII LLHVFWGIVFFDGCEKKW GILLIVLLT  
HLLVSAQTFI SYYGINLASAFI ILVLMGTWAFLAAGGSCRSLKLCLLCQDKNFLYNQR SR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

## **FIGURE 95**

AATTTTCACCAAGAGTAAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTGCCTCGTG  
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTGTCTTAGGATCAAC  
TCGGTCATTACCACAGCTAAACCTGTTGGACTCCCTCCCACAAAACTGGCTCCGGATCAGG  
GAACACTACCAAAACCAACAGCAGTCAAATCAGGTCTTCCTTCTTAAGTCTGATACCATTAAACA  
CAGATGCTCACACTGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC  
CCAGACCCACCCATTGACCCCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC  
CAATTTGTACACAACTTGAGGCCAGGGCACTATCTAAGCTCAGAGGAATTGCCACAAATC  
TTCACGAGCCTCATCATCCATTCTGTTCCGGGAGGCATCCTGCCACCAGTCAGGCAGGGC  
TAATCCAGATGTCCAGGATGGAAGCCTCCAGCAGGAGGAGCAGGTGTAATCCTGCCACCCAGG  
GAACCCAGCAGGCCCTCCCAACTCCAGTGGCACAGATGACGACTTGCAGAGTCACCACCCCT  
GCAGGCATCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA  
GTAAGCTGTTCAAATTTCAAACTAAGCTGCCTCGAATTGGTGATACTGTGAATCTTATC  
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAAATTCTTAATT  
TACCTGAAATATTCTGAAATTTCAGAAATATGTTCTATGTAGAGAATCCAACTTTAAAAAA  
CAATAATTCAATGGATAAAATCTGTCTTGAATATAACATTATGCTGCCTGGATGATATGCATAT  
TAAAACATATTGGAAAACTGGAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 96**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

## FIGURE 97

## **FIGURE 98**

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT  
EGPFAMDPDSGFLLVTRALDREEQAELYQLQVTLEMQDGHVLWGPQPVLHVKDENDQVPHFSQAI  
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPDMFQLEPRLGALALSPKG  
STSLLDHALERTYQLLVQVKDMGDQASGHQATATVEVSIIESTWVSLEPIHLAENLKLYPHHMAQ  
VHWSSGGDVHYHLESHPGPFEVNAEGNLYVTRELDREAQEYLLQVRAQNSHGEDYAAPPLELHVL  
VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSHVYQLLSPEPEDGVGRA  
FQVDPTSGSVTLGVPLRAGQNILLVLAMDLAGAEGGSSTCEVEAVTDINDHAPEFITSQIG  
PISLPEDVEPGTLVAMLTAIDADLEPAFRIMDFAIERGDTETGTFGLDWEPDGHVRLRLCKNLSY  
EAAPSHEVVVVVQSVAKLVGPGPGPATATTVLVERVMPPPQLDQESYEASVPISAPAGSFLLT  
IQPSDPISRTRLFSLVNDSEGWLCLIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALTTLAPVPS  
QYLCTPRQDHGLIVSGPSKDPDIASGHGPYSFTLGPNPVQRDWRLQTLNGSHAYLTLLAHWVEP  
REHIIPVVVSHNAQMWWQLLVRVIVCRCNVQCMRKVGRMKGMPTKLSAVGILVGTVAIGIFLI  
LIFTHWTMSRKDKDPQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

## **FIGURE 99**

GGCTGACCGTGCTACATTGCCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGCC  
AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCACGCTCTGGAAAGCACCGCCTTA  
TCTCTCACCTCAAGTCCCCTTCTCAAGAACATCCTCTGTTCTTGCCTCTAAAGTCTGGTAC  
ATCTAGGACCCAGGCATCTTGCTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAATG  
TTCTCCTTATGTTGGTCTACTATTGCATTAGAAGCTGCAACAAATTCAATGAGACTAGCACC  
TCTGCCAACACTGGATCCAGTGTGATCTCAGTGGAGGCCAGCACAGCCACCAACTCTGGGTCCAG  
TGTGACCTCCAGTGGGTCAAGCACGCCACCATCTCAGGGTCCAGCGTACCTCCAATGGGTCA  
GCATAGTCACCAACTCTGAGTCCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG  
TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACCTCCAGTGG  
GGCCAGCACGCCACCAACTCTGAGTCCAGCACACCCCTCAGTGGGCCAGCACAGTCACCAACT  
CTGGGTCCAGTGTGACCTCCAGTGGAGGCCAGCAGTGCACCAACTCTGAGTCCAGCACAGTGTCC  
AGTAGGGCCAGCAGTGCACCAACTCTGAGTCTAGCACACTCTCAGTGGGCCAGCACAGCCAC  
CAACTCTGACTCCAGCACAAACCTCCAGTGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCAGT  
GCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAG  
AACGACCTCCAATGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACAGCACCTCAGTGGGCCA  
GCACAGGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGCCAGCACACTGCCACCAACTCTGAG  
TCCAGCACGACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG  
GGCTAGCACGCCACCAACTCTGACTCCAGCACAAACCTCCAGTGGGCCAGCACAGCCACCAACT  
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCCTCC  
AGTGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGCCAACACAGCCAC  
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGCCAGCACGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGTCAAGCACGCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGGCCAGCAC  
GCCACCAACTCTGACTCCAGCACAAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCTAG  
CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACAACCTCCAGTGGGCCA  
ACACAGGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGAAACAGCAGCTGACTGG  
ATGCACACAACCTCCATAGTCATCTACTGCAGTGAGTGAGGCAAAGCCTGGTGGGTCCCTGGT  
GCCGTGGAAATCTCCTCATCACCCCTGGTCTCGGTTGTCGGCGGGCGTGGGCTTTGCTGGC  
TCTTCTCTGTGTGAGAACAGGCTGTCCCTGAGAACACCTTAAACACAGCTGTCTACCACCT  
CATGGCCTCAACCATGGCTTGGTCCAGGCCCTGGAGGGAAATCATGGAGCCCCCACAGGCCAG  
GTGGAGCTAACTGGTCTGGAGGAGACCAGTATCATCGATGCCATGGAGATGAGCGGGAGGA  
ACAGCGGGCCCTGAGCAGCCCCGAAGCAAGTGCCGATTCTCAGGAAGGAAGAGACCTGGCA  
CCCAAGACCTGGTTCTTCATTCATCCCAGGAGACCCCTCCAGTTGTTGAGATCTGAA  
AATCTGAAGAAGGTATTCTCACCTTCTGCCTTACAGACACTGGAAAGAGAATACTATAT  
TGCTCATTTAGCTAAGAACATAACATCTCATCTAACACACAGCACAAAGAGAAGCTGTGCTTG  
CCCCGGGTGGGTATCTAGCTGAGATGAACCTAGTTATAGGAGAAAACCTCCATGCTGGACTC  
CATCTGGCATTCAAAATCTCCACAGTAAAATCCAAAGACCTCAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAA

## **FIGURE 100**

MKMQKGNVLLMFGLLLHLEATNSNETSTSANTGSSVISSGASTATNGSSVTSSGVSTATISGS  
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSGASTATNSESSTPSS  
GASTVTNSGSSVTSSGASTATNSESSTVSSRSTATNSESSTLSSGASTATNSDSSTTSSGASTA  
TNSESSTSSGASTATNSESSTVSSRSTATNSESSTTSSGASTATNSESRTTNGAGTATNSES  
STTSSGASTATNSDSTSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNSDSSTTSS  
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA  
TNSESSTTSSGVSTATNSESSTTSSGASTATNSDSTSSEASTATNSESSTVSSGISTVTNSES  
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVVVA  
AVGLFAGLFFCVRNSLSRNTFNTAVYHPHGLNHGLGPAGGGNHGAPHRPRWSPNWFWRPVSSI  
AMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

## **FIGURE 101**

GGCCGGACGCCCTCCCGTTACGGGATGAATTAAACGGGGTCCGCACGGAGGTGTGACCCCTA  
CGGAGCCCCAGCTGCCAACGCACCCCACTCGGCGTCGCGCGCGTGCCTGCTGTACAGGTG  
GGAGGCTGGAACTATCAGGCTAAAAACAGAGTGGGTACTCTCTGGGAAGCTGGCAACAAAT  
GGATGATGTGATATGCATTCCAGGGGAAGGGAAATTGTGGTGCTCTGAACCCTGGTCAATT  
AACGAGGCAGTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAGCTTGGAATCAT  
GGTGTCAAGGAAAGGGATTTACTTATACTGACTCTGTTGGGAAGCTTTGGAAGCATT  
TCATGCTGAGTCCTTACCTTGATGTTGTAACCCATCTGGTATCGCTGGATCAACAAAC  
CGCCTTGTGGCAACATGGCTACCCCTACCTGTGGCATTATTGGAGACCATGTTGGTGTAAAAGT  
GATTATAACTGGGATGCATTGTTCTGGAGAAAGAAGTGTCAATTATCATGAACCCTGGACAA  
GAATGGACTGGATGTTCTGTGAAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT  
TGCCTCAAAGCGAGTCTCAAAGGTGTTCTGGATTGGTGGCCATGCAGGCTGCTGCCTATAT  
CTTCATTCA TAGGAAATGGAAGGATGACAAGAGCCATTGCAAGACATGATTGATTACTTTGTG  
ATATTCA CGAACCACTCACTCCTCATATCCCAGAAGGGACTGATCTCACAGAAAACAGCAAG  
TCTCGAAGTAATGCATTGCTGAAAAAAATGGACTTCAGAAATATGAATATGTTTACATCCAAG  
AACTACAGGCTTACTTTGTGGTAGACCGTCTAAGAGAAGGTAAAGAACCTTGATGCTGTCCATG  
ATATCACTGTGGCGTATCCTACAACATT CCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT  
CCCAGGAAATCCACTTACG TCCACCGGTATCCAATAGACACCCCTCCCCACATCCAAGGAGGA  
CCTTCAACTCTGGGCCACAAACGGTGGAGAGAAAGAAGAGAGGCTGCGTTCTTCTATCAAG  
GGGAGAAGAATT TTTACCGGACAGAGTGTCAATTCCACCTGCAAGTCTGAACTCAGGGTC  
CTTGTGGCAAATTGCTCTATACTGTATTGGACCTGTTCA GGCCTGCAATGTGCCTACTCAT  
ATATTGTACAGTCTGTTAAGGGTATT TATAATCACCATTGTAATCTTGCTGCAAGAGA  
GAATATTGGTGGACTGGAGATCATAGAACTTGCATGTTACCGACTTTACACAAACAGCCACAT  
TTAAATTCAAAGAAAATGAGTAAGATTATAAGGTTGCCATGTGAAAACCTAGAGCATATTG  
GAAATGTTCTAAACCTTCTAAGCTCAGATGCATTTGCATGACTATGTCGAATATTCTTACT  
GCCATCATTATTGTTAAAGATATTGCACTTAATTGTGGAAAAAATTGCTACAATT  
TTAATCTCTGAATGTAATTGATACTGTGTACATAGCAGGGAGTGTACGGGGTGAATAACTT  
GGGCCAGAATATTAAACAATCATCAGGCTTTAAA

## **FIGURE 102**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFGIMVSWKGIYFILTLFWGSFFGSIFMLSP  
FLPLMFVNPSWYRWINNRLVATWLTPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM  
FLWNCLMRYSYLRLKEKICLKLASILKGVPFGWAMQAAAYIFIHRWKDDKSHFEDMIDYFCDIHEP  
LQLLIFPEGTDLTENSRSNAFAEKNGLQKYEYVLHPRTTGFTVVDRREGKNLDLVHDITVA  
YPHNIPQSEKHLLQGDFPREIHFHVRYPIDLPLTSKEDLQLWCHKRWEEKERLRSFYQGEKNF  
YFTGQSVIPPKSELRLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG  
LEIIIELACYRLLHKQPHLNNSKKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

## **FIGURE 103**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCCACGGCTCCTGCGCTGAGACAGCTGGCCTGACC  
TCCAAATCATCCATCCACCCCTGCTGTCACTGTTTCATAGTGTGAGATCAACCCACAGGAATA  
TCCATGGCTTTGTGCTCATTTGGTTCTCAGTTCTACGAGCTGGTGTAGGACAGTGGCAAGT  
CACTGGACCGGGCAAGTTGTCCAGGCCTGGTGGGGAGGACGCCGTGTTCTCTGCTCCCTCT  
TTCTGAGACCAGTGCAAGAGGCTATGGAAGTGCAGGTTCTCAGGAATCAGTTCCATGCTGTGGTC  
CACCTCTACAGAGATGGGAAGACTGGGAATCTAACGAGATGCCACAGTATCGAGGGAGAAGTGA  
GTTGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTCAAGGCTAAAAACATCACTCCCTCGG  
ACATGGCCTGTATGGGTGCTGGTTCAAGTCCCAGATTACGATGAGGAGGCCACCTGGGAGCTG  
CGGGTGGCAGCACTGGGCTCACTCCTCTCATTCCATCGTGGGATATGTTGACGGAGGTATCCA  
GTTACTCTGCCGTGCTCAGGCTGGTCCCCAGGCCACAGCCAAGTGGAAAGGTCCACAAGGAC  
AGGATTGTCTCAGACTCCAGAGCAAATGCAGATGGTACAGCCTGTATGATGTGGAGATCTCC  
ATTATAGTCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTGCTGAGCAGAGTCATGA  
GGTGAATCCAAGGTATTGATAGGGAGAGCAGTTTCCAGGCCACCTGGCGCTGGCTCTA  
TTTACTCGGGTTACTCTGTGGTGCCTGTGTTGATGGGATGATAATTGTTTCTTC  
AAATCCAAGGGAAAATCCAGGGGAACTGGACTGGAGAAAGCACGGACAGGAGAATTGAG  
AGACGCCCGAAACACGCACTGGAGGTGACTCTGGATCCAGAGACGCCACCCGAAGCTCTGCG  
TTTCTGATCTGAAAATGTAACCCATAGAAAAGCTCCCAGGAGGTGCTCACTTGAGAAGAGA  
TTTACAAGGAAGAGTGTGGTGCCTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA  
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTCGGATGACGTAGACAGGGGAAGAACAA  
ATGTGACTTTGTCTCCAAACAATGGGTATTGGTCTCAGACTGACAACAGAACATTGTATTC  
ACATTCAATCCCCATTATCAGCCTCCCCCAGCACCCCTCCTACACGAGTAGGGTCTCCT  
GGACTATGAGGGTGGGACCATCTCTTCTCAATACAATGACCAGTCCCTTATTATACCTGC  
TGACATGTCAGTTGAAGGCTTGTGAGACCTATATCAGCATGCGATGTATGACGAGGAAAG  
GGGACTCCCATATTCAATGTCAGTGTCTGGGATGAGACAGAGAACCCTGCTTAAAGGGC  
CCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCCCGACAGGTGGCCCCAGCTCCCT  
CCGGAGCCTGCGCACAGAGAGTCACGCCCAACTCTCTTAGGGAGCTGAGGTCTCTGCC  
TGAGCCCTGCAAGCGGCAGTCACAGCTCCAGATGAGGGGGGATTGGCCTGACCTGTGGGAG  
TCAGAACCATGGCTGCCCTGAAGTGGGAGCGGAATAGACTCACATTAGGTTAGTTGTAAAA  
CTCCATCCAGTAAGCATTGAAACAAGTCACAACCTCCAGGCTCTCATTGCTAGTCACGG  
ACAGTGATTCTGCTCACAGGTGAAGATTAAAGAGAACAGAACATGTGAATCATGCTGCAGTT  
TGAGGGACAGTGTGTTCTAATGATGTGTTTATATTACATTTCACCATAAAACTCTGTT  
TGCTTATTCCACATTAATTACTTTCTCTACCAATCACCATGGAATAGTTATTGAACACC  
TGCTTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTCACTGATTCTATAAGCCCAGCAT  
TACCTGATAACAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAAGAAACTACAGGTCCATATCC  
CTCATTAACACAGACACAAAAATTCTAAATAAAATTAAACAAATTAAACTAAACAATATTTA  
AAGATGATATATAACTACTGAGTGTGGTTGTCCCACAAATGCAGAGTTGGTTAATATTTAAAT  
ATCAACCAGTGAATTCACTGACATTAATAAGTAAAAAGAAAACCATAAAAAAAAAAAAAA

## **FIGURE 104**

MAFVLILVLSFYELVSGQWQVTGPGKFWQALVGEDAVFSCSLFPETSAEAMEVRRFRNQFHAVVH  
LYRDGEDWESKQMPQYRGRTEFKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR  
VAALGSLPLISIVGYVDGGIQLLCISSLGWFPQPTAKWKGPQGQDLSSDSRANADGYSLYDVEISI  
IVQENAGSILCSIHLAEQSHEVESKVVLIGETFFQPSPWRLASILLGLLCALCGVVMGMIIVFFK  
SKGKIQAELDWRRKHGQAEELRDAKHAVEVTLDPETAHPKLCVSDLKTVTHRKPQEVPHSEKRF  
TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGCRDDVRGKNNVTLSPNNGYWVRLTTEHLYFT  
FNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPYIQHAMYDEEKKG  
TPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

## **FIGURE 105**

CCTTCACAGGACTCTCATTGCTGGTGGCAATGATGTATCGCCAGATGTGGTGAGGGCTAGGAAAAGAG  
TTTGGTGGAAACCCTGGTTATCGCCTCGTCATCTCATATCCCTGATTGTCCTGGCAGTGTGCATTGGA  
CTCACTGTTCAATTATGTGAGATATAATCAAAGAACCTACAATTACTATAGCACATTGTCATTACAC  
TGACAAACTATATGCTGAGTTGGCAGAGAGGCTCTAACATTACAGAAATGAGCCAGAGACTTGAAT  
CAATGGTAAAAATGCATTTATAAATCTCCATTAAAGGAAGAATTGTCAAGTCTCAGGTTATCAAGTTC  
AGTCAACAGAACGATGGAGTGTGGCTCATATGCTGTTGATTGTAGATTCACTCACTGAGGATCCTGA  
AACTGTAGATAAAATTGTCACATTGTTTACATGAAAGCTCAAGATGCTTAGGACCCCCCTAAAGTAG  
ATCCTCACTCAGTTAAAATTAAAAAAATCAACAAGAACAGAACAGCTATCTAAACCATGCTGCCGA  
ACACGAAGAAGTAAAACCTAGGTCAAGTCTCAGGATCGTGGTGGACAGAAAGTAGAAGAGGGTGAATG  
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGAGTCATCGCTGGAGCAACCTTAATTAAATGCCACATGGC  
TTGTGAGTGCTGCTCACTGTTTACAACATATAAGAACCTGCCAGATGGACTGCTCCCTGGAGTAACA  
ATAAAACCTCGAAAATGAAACGGGTCTCGGAGAATAATTGTCATGAAAATACAAACACCCATCACA  
TGACTATGATATTCTCTTGAGAGCTTCTAGCCCTGTTCCCTACACAAATGCACTAGATAGAGTTGTC  
TCCCTGATGCATCCTATGAGTTCAACCAGGTGATGTGATGTTGTGACAGGATTGGAGCACTGAAAAAT  
GATGGTTACAGTCAAACATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACC  
TCAAGCTTACAATGACGCCATAACTCTAGAATGTTATGTCAGGCTCCCTAGAAGGAAAACAGATGCA  
GCCAGGGTCACTGGAGGACCACTGGTAGGTTAGTCAGATGCTAGAGATATCTGGTACCTGCTGGAATAGTG  
AGCTGGGGAGATGAATGTGCGAAACCCAACAAGCCTGGTGTAACTAGAGTTACGGCCTGGGACTG  
GATTACTCAAAAATGGTATCTAAGAGACAAAGCCTCATGGAACAGATAACATTGTTGGTTGTTG  
GGTGTGGAGGCCATTAGAGATAACAGAATTGGAGAAGACTGCAAAACAGCTAGATTGACTGATCTCA  
ATAAAACTGTTGCTGATGCATGTATTCTTCCAGCTCTGTCAGTAAGCATCCTGCTTGTGCCA  
GATCAACTCTGTCTGTGAGCAATAGTTATGTCATAGAGAAATAGATAATACAATATTAC  
ATTACAGCCTGTATTCTAGAAGTTGTCAGAATTGACTTGTGACATAAATTGTAAT  
GCATATATACAATTGAAGCACTCCTTCTCAGTCCTCAGCTCCTCTCATTCAGCAAAATATCCATT  
TCAAGGTGCAAGAACAGGAGTGAAAGAAAATATAAGAAGAAAAATCCCCTACATTATTGGCACAGAA  
AAAGTATTAGGTGTTCTTAGTGGAAATTAGAAATGATCATATTCAATTGAAAGGTCAAGCAAAGACA  
GCAGAATACCAATCACTCATCTAGAAGTATGGAACTAAGTTAAGGAAGTCCAGAAAGAACCAAG  
ATATATCCTTATTTCATTTCAAACAAACTACTATGATAATGTGAAGAAGATTCTGTTTTGTGACCT  
ATAATAATTATAACAACTTCATGCAATGTACTTGTCTAACGAAATTAAAGCAAATTATTAAACATTG  
TTACTGAGGATGTCAACATATAACAAATAAAATATAACCCCA

## **FIGURE 106**

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTvhYvRynQKKTNYYSTLSFTTDKLY  
AEFGREASNNFTEMSQRLESMVKNAYKSPLREEFVKSQVIKFQQKHGVLAHMLLICRFHSTED  
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG  
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKGRL  
RRIIVHEKYKHPHSDYDISLAELSSPVPTNAVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS  
QNHLRQAQVTLIDATTNEPQAYNDAITPRMLCAGSLEGKTDACQGDGGPLVSSDARDIWYLAG  
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

## **FIGURE 107**

AGAGAAAGAAGCGCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCGCGAAGAAGTTCCCTG  
CCCCGATGAGCCCCCGCGTGCCTCCCGACTATCCCCAGGCAGGCGTGGGGCACCGGGCCCAGC  
GCCGACGATCGCTGCCGTTTGCCTTGGGAGTAGGATGTGGTGAAGGATGGGGCTTCTCCCT  
ACGGGGCTCACAAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCACGCCCTCAA  
TCGCTCTTGGTTAATGTCATCAGTGTGGCAGTTCTGCTGGATGAGGGACTACCTAA  
ATAATGTTCACTTTAACGAGGGTAGAGGAAGCAGTCATTTGACTTACTTTCT  
GTGGTTATCCGGTCATGATTGCTGTTGCTGTTCTTATCATTGTTGGGATGTTAGGATATTG  
TGGACGGTAAAAGAAATCTGTTGCTTGCATGGTACTTGGAGTTGCTGTCAATTCT  
GTGTAGAACTGGCTTGTGGCAGGGACATATGAACAGGAACCTTATGGTCCAGTACAATGGTCA  
GATATGGTCACTTGAAAGCCAGGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA  
TGGTGAATTTTTTCAGAGAGAGTTAACGAGTAGTGTGGAGTAGTATATTCACTGACTGGTGG  
AAATGACAGAGATGGACTGGCCCCCAGATTCTGCTGTTAGAGAATTCCAGGATGTTCCAAA  
CAGGCCACCCAGGAAGATCTCAGTGACCTTATCAAGAGGGTTGTGGAAGAAAATGTTACCTT  
TTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTCTGGGAATCTCCATTGGGGTGACACAAA  
TCCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTTATTATGATAGAAGGGAGCCTGGG  
ACAGACCAAATGATGTCCTTGAAGAATGACAACCTCAGCACCTGTCATGTCCTCAGTAGAACT  
GTTGAAACCAAGCCTGTCAAGAATCTTGACACACATCCATGGCAACAGCTTAATACACACT  
TTGAGATGGGGAGTTAAAAAGAAAATGTCACAGAAGAAAACCACAAAACTTGTGTTATTGGACT  
TGTGAATTGGAGTACATACTATGTTTCAAGAAATATGAGAAATAAAATGTTGCCATAAAA  
TAACACCTAACGATACATACTATTCTATGCTTAAATGAGGATGGAAAAGTTCATGTCATAAGTC  
ACCACCTGGACAATAATTGATGCCCTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC  
TGTGATGACTTTACTGAACACAGTTATGTTTGGCAGCATGGTTGATTAGCATTCCGCA  
TCCATGCAAACGAGTCACATATGGGGACTGGAGCCATAGTAAAGGTTGATTACTTACCAA  
CTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTATTA  
CTCAGCGATCTATTCTCTGATGCTAAATAATTATATCAGAAAACCTTCAATATTGGTGA  
ACCTAAATGTTGATTTTGCTGGTTACTAAATATTCTTACCACTAAAGAGCAAGCTAACACAT  
TGTCTTAAGCTGATCAGGGATTGGTATATAAGCTGTGTTAAATCTGTATAATTCACTGAT  
TTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAATTGTCCTGTATAGCATCATT  
ATTTTACGCTTCTGTTAATAAAGCTTACTATTCTGCTCTGGGCTTATATTACACATATAAC  
TGTATTTAAATCTAACACTAATTGGAAAATTACCACTGATGATACATAGGAATCATTAC  
AGAATGTTAGTCTGGCTTTAGGAAGTATAAAGAAAATTGCACATAACTTAGTTGATTCA  
AAGGACTGTATGCTGTTTCTCCAAATGAAGACTCTTTGACACTAAACACTTTAAAAA  
GCTTATTTGCCTCTCCAAACAAGAAGCAATAGTCTCAAGTCATATAAATCTACAGAAAA  
TAGTGTCTTTCTCCAGAAAATGTTGAGAATCATTAAACATGTGACAATTAGAGATT  
CTTTGTTTATTCTACTGATTAATATACTGTGGCAAATTACACAGATTATAAATTTTACAA  
GAGTATAGTATATTGAAATGGAAAAGTGCATTACTGTATTGTTGATTTGTTAT  
TTCTCAGAATATGAAAGAAAATTAAATGTCATAAAATATTCTAGAGAGTAA

## **FIGURE 108**

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTATAETRVEEAVILTYFPVVHP  
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT  
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREFPGCSKQAHQ  
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTLLWALYYDRREPGTDQM  
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

## **FIGURE 109**

CCAAGGCCAGAGCTGTGGACACCTTATCCCACCTCATCCTCATCCCTCTGATAAAGCCCCTACCAAGTGCT  
GATAAAAGTCTTCTCGTAGAGGCCTAGAGGCCTAAAAAAAAAAAGTGCCTGAAAGAGAAGGGGACAAGGAACA  
CCAGTATTAAGAGGATTTCAGTGTCTGGCAGTTGGTCCAGAAGGGATGCCTCCATTCTGCTTCTCACCTG  
CCTCTTCATCACAGGCACCTCCGTGTCAACCGTGGCCCTAGATCCTGTTCTGTTACATCAGCCTGAATGAGC  
CCTGGAGGAACACTGACCACCAAGTGGATGAGTCTCAAGGCTCCTCTATGTGACAACCAGTGAATGGGAG  
TGGTACCACTTCACGGCATGGCGGGAGATGCCATGCCTACCTCTGCATACCAAGAAAACACTGTGGAACCCA  
CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCGACGGCATTGTGCAACGCCAGGTTGTGCCAGCT  
TCAATGGAACTGCTGTCTGGAACACCACGGTGGAAAGTCAGGCTTGCCCTGGAGGCTACTATGTGTATCGT  
CTGACCAAGCCCAGCGTCTGCTTCCACGCTACTGTGGTCAATTATGACATCTGCGACGGAGACTGCCATGG  
CAGCTGCTCAGATACCAGCGAGTGACATGCGCTCAGGAACGTGCTAGGCCCTGACAGGAGACATGCTTG  
ATGAAAATGAATGTGAGCAAACAGGTGGCTGAGTGAGATCTGTGTGAACCTCAAAACTCCTACCGCTGT  
GAGTGTGGGTTGGCCCTGTGCTAAGAACAGTGTGAAGACGTTGAAGGATGCCACAATAACAA  
TGGTGGCTGCAGCCACTCTGCTTGGATCTGAGAAAGGCTACCAAGTGTGAATGTCCCCGGGCCTGGTGTGT  
CTGAGGATAACCACACTTCCAAGTCCCTGTGTTGCAAATGCCATTGAACTGAACATCCCCAGGGAG  
CTGGTTGGTGGCCTGGACCTCTTCCGACCAACACCTCCTGCCGAGGAGTGTCCAACGGCACCCATGTCAACAT  
CCTCTCTCTCAAGACATGTGGTACAGTGGTCATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA  
CAGGTCTACCCAAGCAGACCCGGGGAGCAGCGGGGACTTCATCATCGAACAGCAAGCTGCTGATCCCAGGT  
ACCTGCGAGTTCCACCCCTGTACACCAATTCTGAAGGATACGTTCCAACCTTCGAAACTCCCCACTGGAAAT  
CATGAGCCGAAATCATGGATCTTCCATTCACTCTGGAGATCTCAAGGAAATGAGTTGAAGAGCCTTACC  
GGGAAGCTCTGCCACCCCTCAAGCTTGTGACTCCCTACTTGGCATTGAGCCCTGGTGCACGTGAGCCG  
TTGGAAAGCTTGGTGGAGAGCTGTTGCCACCCACCTCCAAGATCGACGAGGTCTGAAATACTACCTCAT  
CCGGGATGGCTGTGTTAGATGACTCGTAAAGCAGTACACATCCGGATCACCTAGCAAAGCACTTCCAGG  
TCCCTGTCTCAAGTTGTGGCAAAGACCACAAGGAAGTGTCTGACTGCCGGTCTTGTGTGGAGTG  
TTGGACGAGCTTCCCGCTGTGCCAGGGTTGCCACCCGGCGAATGCGTGTGGGAGGAGGACTCAGC  
CGGTCTACAGGCCAGCGCTAACAGCGGCCGATCCGATCGACTGGAGGACTTAGTTGTAGCCATACCTC  
GAGTCCCTGCATTGGACGGCTGCTTTGGAGCTTCTCCCCCACCAGCCCTCTAAGAACATCTGCCAACAGC  
TGGGTTCAAGACTCACACTGTGAGTTAGCTCCACCAACTCACTCTGATTCTGGTCCATTCAAGTGGCA  
CAGGTCTACAGCACTGCTGAACAATGTGGCTGGGTGGGTTCTTCTAGGGTTGAAACTAAACTGTCCA  
CCCAGAAAGACACTCACCCATTCCCTATTCTTCACTTAAACACCTCGTGTATGGTCAACAGAC  
CACAAAATCAGAAGCTGGGTATAATATTCAAGTACAAACCTAGAAAAATTAAACACTTACTGAAATTATGA  
CTTAAATACCAATGACTCCTAAATATGTAATTAGTTACCTTGAATTCAATTCAAATGCAGACTAA  
TTATAGGGAATTGGAAGTGTATCAATAAAACAGTATATAATT

## **FIGURE 110**

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFTGMAGDAMP  
TFCIPEHCGTHAPWLNGSHPLEGDGIVQRQACASFNGNCCLWNNTTVEVKACPGGYYVYRLTKPSVCFHV  
YCGHFYDICDEDCHGCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV  
LRSRGKTCEDVEGCHNNNGGCSHSLGSEKGYQCECPRLVLSEDNHTCQPVVLCKSNAIEVNIPRELVGG  
LELFLTNTSCRGVSNGLTHVNILFSIKTCGTVVVDVNDKIVASNLVTGLPKQTGSSGDFIIRTSKLLIPVT  
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEEPYREALPTLKLRSLSYFGIEPVVHV  
SGLESLVESCFATPTSKIDEVLKYLIIRDGCVSDDSVKQYTSRDHLAKHFQVVFVFKVGKDHEVFLHCRV  
LVCGVLDERSRCAQGCHRRMRRGAGGEDSAGLQGQTLTGGPIRIDWED

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

**Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

**N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537

**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

**ZP domain proteins.**

amino acids 431-457

**Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

## **FIGURE 111**

GAGAGAGGCAGCAGCTGCTCAGCGGACAAGGATGCTGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG  
GCCTCCTCCAGCCAGTGTGACCAGGGACTTCTGACCTGCTGCCAGCCAGGACCTGTGTGGGAGGCCCT  
CCTGCTGCCCTGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGGCCAGC**ATGT**  
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGAAACCCGTATCCCC  
ATGGAGACCTTCAGAAAGGTGGGATCCCCATCATCATAGCACTACTGAGCCTGGCAGGTATCATATTGT  
GGTTGTCCATCAAGGTGATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCGA  
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC  
CCCAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTGGCAC  
AGGGAACTGGTCTGCCTGTTGACAACCTCACAGAACGCTCTCGTGAGACAGCCTGTAGGCAGATGG  
GCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGATGTTGAAATCACAGAAAACAGCCAG  
GAGCTTCGCATGCGGAACCTCAAGTGGCCCTGTCCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTG  
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGCTCTACGGCA  
GCCCACTGCTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGCAG  
CTTCCCATCCCTGGCTGTGGCCAAGATCATCATATTGAATTCAACCCATGTACCCAAAGACAATGACA  
TCGCCCTCATGAAGCTGCAGTCCCACACTTTCTCAGGCACAGTCAGGCCATCTGCTGCCCTCTT  
GATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATGGATGGGCTTACGAAGCAGAATGGAGGAA  
GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTATTGACAGCACACGGTGAATGCAGACGATGCGT  
ACCAGGGGAAGTCACCGAGAAGATGATGTGTGAGGCATCCCGAAGGGGTGTGGACACCTGCCAGGGT  
GACAGTGGTGGGCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGCATCGTAGCTGGCTATGG  
CTGCGGGGGCCCGAGCACCCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT  
GGAAGGCTGAGCTG**TAAT**GCTGCTGCCCTTGTGAGCTGCTGGAGGCCCTCCCTGCCACCT  
GGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCCCTGGTACACCCCTCTGCCACAGCCTCAGCAT  
TTCTGGAGCAGCAAAGGGCTCAATTCTGTAAGAGACCCCTCGCAGCCAGGGCGCCAGAGGAAGTCA  
GCAGCCCTAGCTCGGCCACACTTGGTGTCTCCAGCATCCCAGGGAGAGACAGCCCAGTGAACAAGGTCT  
CAGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTGTAAAAGCC  
CAGATCACTGTGGCTGGAGAGGAGAAGGAAGGGCTGCGCCAGCCCTGTCGTCTCACCCATCCCCAA  
GCCTACTAGAGCAAGAAACCAAGTGTAAATATAAAATGCACTGCCCTACTGTGGTATGACTACCGTTACCT  
ACTGTTGTCATTGTTATTACAGCTATGCCACTATTATAAGAGCTGTGTAACATCTCTGGCAAAAAAAA  
AAAA

## **FIGURE 112**

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIP III ALLSLASIIIVVVLIKVILDKYFLCG  
QPLHFIPRKQLCDGELDCPLGEDEEHCVKS FPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN  
FTEALAEATACRQMGSRAVEIGPDQDLDVVEITENSQEIRMRNSSGPCLSGSLVSLHCLACGKSL  
KTPRVVGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKL  
GSFPSLAVAKIIIIIFNPMPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWG  
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTQCQGDGGPLMYQS  
DQWHVVVGIVSWGYZGCZGPSTPGVYTKVSAYLNWIYNVWKEL

**Transmembrane domain:**

amino acids 32-53 (typeII)

### **FIGURE 113**

GGCTGGACTGGAACCTCTGGTCCAAGTGATCCACCCGCCCTCAGCCTCCCAAGGTGCTGTGATTA  
TAGGTGTAAGCCACCGTGTGGCCTCTGAACAACCTTTTCACTAAGCAACTAAAAAGCCACAGGAGT  
TGAAC TGCTAGGATTCTGACTATGCTGTGGCTAGTGCTCCTACTCCTACCTACATTAAAATC  
TGTTTTTGTCTCTGTAACTAGCCTTACCTCCTAACACAGAGGATCTGTACTGTGGCTCT  
GGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTCTACCACACCGTCCCCTCGAAG  
CCGGGGACAGCCTCACCTGCTGGCCTCTCGCTGGAGCAGTGCCCTACCAACTGTCTACGTCT  
GGAGGCAGTGACTCGGGCAGTGAGCTGAGCCTCTGGTAGCTGCGGCTTCAGGTGGC  
CTTGCCCTGGCGTAGAAGGGATTTGACAAGCCCCGAAGATTTCATAGGCGATGGCTCCCACTGCC  
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGCCAGGACGGCCGTGGACACCTGCTCA  
GAAGCAGTGGGTGAGACATCACCGCTGCCGCCATCTAACCTTTCATGTCCTGCACATCACCTG  
ATCCATGGGCTAATCTGAACTCTGCTCCAAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC  
CAGAAGGGGTCTGCTTAGACCACCTGGTTATGTGACAGGACTTGCAATTCTCTGGAACATGAGG  
GAACGCCGAGGAAAGCAAAGTGGCAGGGAAAGGAACCTTGCCAAATTATGGGTAGAAAAGATG  
GAGGTGGGGTTATCACAAGGCATCGAGTCTCCTGCATTCACTGAGCTGAGCTGTGGCTCAGACC  
CCGATGGCGCATGACACACTCGGACTCACCTCTGGGCCATCAGACAGCCGTTCCGCCCGAT  
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA  
TCTGCGATCACCAGCCAGGGCAGCGTCTGGGAAGGAGCAAGCAAAGTGACCTTCTCTCCC  
CTCCTCCCTCTGAGAGGCCCTCTATGTCCTACTAAAGCCACAGCAAGACATAGCTGACAGG  
GGCTAATGGCTCAGTGTGGCCAGGAGGTAGCAAGGCCCTGAGAGCTGATCAGAACAGGCTGCT  
GTGCGAACACGGAAATGCCCTCAGTAAGCACAGGCTGCAAATCCCCAGGCAAAGGACTGTGTGG  
CTCAATTAAATCATGTTAGTAATTGGAGCTGTCCCCAAGACCAAGGAGCTAGAGCTTGGTT  
CAAATGATCTCCAAGGGCCCTATAACCCAGGAGACTTTGATTGAAATTGAAACCCCCAAATCCA  
AACCTAAGAACCGAGGTGCAATTAGAACATCAGTTATTGCCGGGTGTGGCTGTAATGCCAACAT  
TTTGGGAGGCCAGGCCGGTAGATCACCTGAGGTAGGAGTTCAAGACCAAGGCCCTGGCAACATGG  
TGAAACCCCTGTCTACTAAAAAATACAAAAAAACTAGCCAGGCATGGTGGTGTGCCTGTATC  
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAAACCTGGGAGGTGAAGGAGGCTGAGACA  
GGAGAACATTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATTA  
TGGTTATTTGTAA

## **FIGURE 114**

MLWWLVLLLLPTLKVFCSLVTSLYLPNTEDSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC  
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRD

**Signal peptide:**

amino acids 1-15

## **FIGURE 115**

CAGCAGTGGCTCTCAGCCTCTAAAGCAAGGAAAGACTGTGTGCTGAGAGACCATGGCAA  
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAACGCTTTAAATCCAAGAAA  
ATATGTAAATCACTTAAGATTGTGGACTGGTGTGGTATCCTGGCCCTAACTCTAATTGTCC  
GTTTGCCCCAGCAAGCAACTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT  
TCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAACTGAAATA  
TTCAGAAGCGGAAATGGCATGATGAAACATTGGAAGTGCACGACTTAAACGGATAACTGG  
CATCTACTTCGTGGGTCTC**AAAATGTTTATC**AAACTCAGATTAAAGTGATTCTGAATTTT  
CTGAACCAGAAGAGGAATAGATGAGAATGAAGAAATTACCAACTTCTTGAACAGTCAGTG  
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAACCGAGATTTCCTTAAAAATTCCAAATTCTGGA  
GATTGGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTCTGAGTTACAG  
ACTTGAGGAGGAGGGAGAAGATCTCACTTCCTGCCAACGAAAAAAAAGGGATTGAACAAAAT  
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGA  
AGAAACTTCAATAAATGACTATACTGAAATAGAATTGATCCCATGCTGGATGAGAGAG  
GTTATTGTTGTATTACTGCCGTGAGGCAACCGCTATTGCCGCCGCTGTGAACTTACTA  
GGCTACTACCCATATCCATACTGCTACCAAGGGAGGACGAGTCATCTGCGTGTCATATGCCTT  
TAACTGGTGGGTGGCCCGCATGCTGGGAGGGCTAAATAGGAGGTTGAGCTCAAATGCTTAAAC  
TGCTGGCAACATATAAAATGCATGCTATTCAATGAATTTCTGCCCTATGAGGCATCTGCCCT  
GGTAGCCAGCTCTCCAGAATTACTGTAGGTAATTCCTCTTCATGTTCTTAAAAACTTCTACA  
TTATCACCAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 116**

MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTLLIVLFWGSKHFWPEVPKKAYDME  
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP  
EFSEPEEEIDENEETTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSE  
LQDFEEEEDLHFPAKEKKGIEQNEQWVVPQVKVEKTRHARQASEEEELPINDYTENGIEFDPMED  
ERGYCCIYCRRGNRYCRRVCEPLLGYYPYPCYQGGRVICRVIMPCNWWVARMLGRV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-  
242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

## **FIGURE 117**

GAGCTCCCTCAGGAGCGCGTTAGCTTCACACCTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCAGCA  
GGCGGGCGGCCAGGATCATGTCACCACACCACATGCCAAGTGGTGGCGTCCCTGTCCATCCTGGGCT  
GGCGGCTGCATCGCGCCACCGGGATGGACATGTGGAGCACCAGGACCTGTACGACAACCCGTACCT  
CCGTGTTCCAGTACGAAGGGCTGAGGAGCTGCGTGAGGCAGAGTTCAGGCTCACCGAATGCAGGCC  
TATTCACCATCCTGGACTTCAGCCATGCTGCAGGCAGTGCAGGCCGTATGATCGTAGGCATCGTCC  
GGGTGCCATTGGCCTCTGGTATCCATCTTGCCTGAAATGCATCCGATTGGCAGCATGGAGGACTCTG  
CCAAAGCCAACATGACACTGACCTCCGGATCATGTTCAATTGCTCAGGCTTGTGCAATTGCTGGAGTG  
TCTGTGTTGCCAACATGCTGGTACTAACCTGGATGTCACAGCTAACATGTACACCGGCATGGTGG  
GATGGTGCAGACTGTTAGACCCAGGTACACATTGGTGCAGGCTCTGTTGCTGGCTGGCTGGAGGCC  
TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGCTGGCACAGAAGAAACCAACTACAAA  
GCCGTTCTTATCATGCCCTCAGGCCACAGTGGTGCCTACAAGCCTGGAGGCTCAAGGCCAGCACTGGCTT  
TGGGTCCAACACCAAAACAAGAAGATAACGATGGAGGTGCCGCACAGAGGACGAGGTACAATCTTATC  
CTTCCAAGCAGCACTATGTTAATGCTTAAGACCTCTCAGCACGGCGGAAGAAACTCCGGAGAGCTCA  
CCCCAAAAACAGGAGATCCCCTAGATTCTCTTGCTTTGACTCACAGCTGGAAAGTTAGAAAAGCCT  
CGATTTCATCTTGGAGAGGCCAAATGGTCTAGCCTCAGTCTGTCTAAATATTCCACCATAAAACA  
GCTGAGTTATTTATGAATTAGAGGTATAGCTCACATTTCATCCTCTATTCTTTAAATAACT  
TTCTACTCTGATGAGAGAATGTGGTTAATCTCTCTCACATTGATGATTTAGACAGACTCCCCCTC  
TTCCTCTAGTCAATAAACCCATTGATGATCTATTCCAGCTTACCCCAAGAAAACCTTGAAGGAAA  
GAGTAGACCCAAAGATGTTATTTCTGCTGTTGAATTGCTCCCCACCCCAACTTGGCTAGTAATAA  
ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATTGTAATCTCTCCAGCCCATGATCTGGTTTCTT  
ACACTGTGATCTTAAAGTTACCAAACCAAAAGTCATTTCAGTTGAGGCAACCAACCTTCTACTGCTG  
TTGACATCTCTTATTACAGCAACACCATTCTAGGAGTTCTGAGCTCTCCACTGGAGTCTTCTGT  
CCGGGGTCAGAAATTGCTCTAGATGAATGAGAAAATTATTTTTAATTAAAGTCCTAAATATAGTTAA  
AATAAATAATGTTTAGTAAATGATAACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG  
GAAATGAAAAATAATTGCTTGAATTGACTATGTCTATATGGTACTTGTAAAGTCATGCTTAAGTACAATTCC  
ATGAAAAGCTCACACCTGTAATCTAGCATTGGAGGCTGAGGAGGAAGGATCACTTGAGGCCAGAAGT  
TCGAGACTAGCCTGGCAACATGGAGAAGCCCTGTCTCACAAATACAGAGAGAAAATCAGCCAGTCA  
TGGTGGCATAACACTGTAGTCCCAGCATTCCGGAGGCTGAGGTGGGAGGATCACTTGAGGCCAGGGAGGT  
TGGGGCTGCAGTGACCCATGATCACACCACTGCACCTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA  
AATAAAAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCTTAA

## **FIGURE 118**

MSTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTECRP  
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSI FALKCIRIGSMEDSAKANMTLTSGIMFIVSGL  
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGVWVAGGLTLIGGVMMCIA  
CRGLAPEETNYKAVSYHASGHHSVAYKPGGFCASTGFGSNTKNKKIYDGGARTEDEVQSYP SKHDY  
V

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

## **FIGURE 119**

GGAAAAACTGTTCTCTCTGTGGCACAGAGAACCTGCTCAAAGCAGAAGTAGCAGTCCGGAGTCC  
AGCTGGCTAAACTCATCCCAGAGGATAATGGCAACCCATGCCTAGAAATCGCTGGCTGTTCTTG  
GTGGTGTGGAATGGTGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTGGCCTTCATT  
GAAAACAACATCGTGGTTTGAAACTTCTGGAAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA  
CATCAGGATGCAGTCAAATCTATGATTCCCTGCTGGCTTTCTCCGGACCTACAGGCAGGCCAGAG  
GACTGATGTGCTGCTCCGTGATGCTCTTGGCTTCATGATGGCCATCCTGGCATGAAATGC  
ACCAGGTGCACGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT  
CATCACGGGCATGGTGGTGCTCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTCTATA  
ACTCAATAGTGAATGTTGCCAAACAGTGAGCTGGAGAAGCTCTACTTAGGATGGACCACGGCA  
CTGGTGCTGATTGTTGGAGGAGCTGTTCTGCGTTTTGCAACGAAAGAGCAGTAGCTA  
CAGATACTCGATACACCTTCCCATCGACAACCCAAAAAGTTATCACACCGAAAGAAGTCACCGAGCG  
TCTACTCCAGAAGTCAGTATGTGTAGTTGTATGTTTAACTTACTATAAACCCATGCAAATG  
ACAAAAATCTATATTACTTCTCAAATGGACCCAAAGAAACTTGAATTACTGTTCTTAACTGCCT  
AATCTTAATTACAGGAACTGTGCATCAGCTATTGATTCTATAAGCTATTCAGCAGAAATGAGATA  
TTAAACCAATGCTTGATTGTTCTAGAAAGTATAGTAATTGTTCTAAGGTGGTCAAGCATACTA  
CTCTTTTATCATTACTTCAAATGACATTGCTAAAGACTGCATTATTTACTACTGTAATTCTCC  
ACGACATAGCATTATGTACATAGATGAGTGTAAACATTATCTCACATAGAGACATGCTTATATGGT  
TTTATTTTAAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTAGGGAA  
ATCATGGATAGGGTTGAAGAAGGTTACTATTAAATTGTTAAAACAGCTTAGGGATTATGCTCCA  
TTTATAATGAAGATTAAGGTTAAATGAAGGCTTAATCAGCATTGTAAGGAAATTGAATGGCTTCTGATAT  
GCTGTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTATCCTCTCCAGAGGCTTTTT  
CTTGTGTTAAATTAACATTGTTAAACAGCAGATATTGTCAGGGCTTTGCATTCAAACGCTT  
TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGTGTTAGGAAAGTG  
AAAATATTTTGTTGTATTGAGAAGAAGATGATGCATTGACAAGAAATCATATATGTATGGAT  
ATATTTTAATAAGTATTGAGTACAGACTTGAAGGTTCATCAATATAAAAGAGCAGAAAATA  
TGTCTGGTTTCATTGCTTACCAAAAAACAAACAAAAAGTTGCTCTTGAAGAAACTCACCT  
GCTCCTATGTGGGTACCTGAGTCAAATTGTCATTGTTCTGTGAAAATAAATTCCCTCTGTA  
CCATTTGTTAGTTACTAAATCTGAAATACTGTATTGTTCTGTTATTCAAATTGATGAA  
ACTGACAATCCAATTGAAAGTTGTGTCGACGTCTGTCTAGCTAAATGAATGTGTTATTGCTT  
TATACATTTATTAATAAAATTGTACATTGTTCTAATT

## **FIGURE 120**

MATHALEIAGLFLLGGVGMVGTVAVTVMPOWRVSIFIENNIVVFENFWEGLWMNCVRQANIRMOCK  
IYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMMKCTRCTGDNEKVKAHILLTAGIIFIITG  
MVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY  
RYSIPSHRTTQKSYHTGKKSPSVYRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

## **FIGURE 121**

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCCTGCCGCGCCTCGGAGCGCGGCGAG  
CCAGACGCTGACCACGTTCCCTCCTCGGTCTCCTCCGCCCTCCAGCTCCGCGCTGCCCGCAGCC  
GGGAGCCATGCGACCCCAGGGCCCCGCCGCCCTCCCGCAGCGGCTCCGCCCTCGCTGCTCC  
TGCTGCTGCAGCTGCCCGCCGTCAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAGGCGCAG  
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC  
TGGTCGAGACGGGAGCCCTGGGCCAATGTTATTCCGGTACACCTGGATCCCAGGTGGATG  
GATTCAAAGGAGAAAAGGGGAATGCTGAGGGAAAGCTTGAGGAGTCCTGGACACCCAAC  
AACAGCTGTTCATGGAGTTCAATTGAATTATGGCATAGATCTGGAAAATTGCGGAGTG  
TACATTACAAGATGCGTTCAAATAGTGCCTAAGAGTTTGTTCACTGGCTACTCGCTAAAATGCA  
GAAATGCATGCTGTCAGCGTTGGTATTCACATTCAATGGAGCTGAATGTTCA  
GGACCTCTTCCCATTGAAGCTATAATTATTGGACCAAGGAAGCCCTGAAATGAATTCA  
ACAATTAAATTATCGCACTTCTCTGTGGAAGGACTTGTGAAGGAATTGGTGTGGATTAGTGG  
ATGTTGCTATCTGGTTGGCACTTGGTCAAGATTACCCAAAAGGAGATGCTTCA  
CTGGATGGAATTCACTGGTCTACTGGATGGAATTCACTGGTCTACTGG  
ATTATTGAAGAACTACCAAAATAATGCTTAATTTCATTTGCTACCTCTTTTATTATGCC  
TTGGAATGGTCACTAAATGACATTAAAGTTATGTATACTGAATGAAAAGCAAAG  
CTAAATATGTTACAGACCAAAGTGTGATTCACACTGTTAAATCTAGCATT  
ATTGCTCAATCAAAAGTGGTTCAATATTTTTAGTTGTTAGAATACTTCTTCA  
TAGTCACATTCTCTCAACCTATAATTGGAATTGTTGTTAGTCTTCTTCT  
AAAAAAATATAAAAAGCTACCAATCTTGACAATTGTAAATGTTAAGAATT  
TTTTTATATCTGTTAAATAAAATTATTCCAACA

## **FIGURE 122**

MRPQGPAAASPQRRLGLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGR  
DGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK  
MRSNSALRVLFSGSIRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMNSTINIHRTS  
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

## **FIGURE 123**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCCTGCCCTGGGCTCCAACGCAGCTGTGGCTGAA  
CTGGGTGCTCATCACGGGAACGTGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA  
ATTGCCTGGAAGAATACATCATGTTTCGATAAGAAGAAAATTGTAAGGATCCAGTTTTTTTA  
ACCGCCCCCTCCCCACCCCCCAAAAAACTGAAAGATGCAAAACGTAATATCCATGAAGATCC  
TATTACCTAGGAAGATTGATGTTGCTGCGAATGCCGTGTTGGATTATTTGTTCTTGAG  
TGGTCTGCGTGGCTGGCAAAGAATAATGTTCAAATCGGTCCATCTCCAAGGGTCCAATT  
TCTTCTGGGTGTCAGCAGCCCTGACTCACTACAGTCAGCTGACAGGGCTGTCATGCAACTG  
GCCCTAAGCAAAGCAAAAGACCTAAGGACGACCTTGAACAATACAAAGGATGGGTTCAATG  
TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTAGGCCCACTGCTTACTGACAATG  
CTTCTCTGCCGAACGAGGATGCCCTAACGGCTGAGGTGAGGCAAATGGTATATTGTGA  
ATCTCAGAAATTACAGGAGATACCCCTCAAGTATATCTGCTGGTTGCTTAGGTTGCCCCTCGCT  
ATAACAGCCTCAAAACTTAAGTATAATCAATTAAAGGGCTAACCGAGCTCACCTGGCTATAC  
CTTGACCATAACCATATCAGCAATTGACGAAATGCTTTAATGGAATACGCAGACTCAAAGA  
GCTGATTCTAGTTCCAATAGAATCTCTATTCTTAACAAATACCTCAGACCTGTGACAAATT  
TACGGAACCTGGATCTGCTCTATAATCAGCTGCATTCTGGGATCTGAACAGTTGGGGCTTG  
CGGAAGCTGCTGAGTTACATTACGGCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCA  
AGACTGCCGCAACCTGGAACCTTGGACCTGGGATATAACCGGATCCGAAGTTAGCCAGGAATG  
TCTTGCTGGCATGTCAGACTCAAAGAACCTCACCTGGAGCACAACTCAATTTCAGCTAAC  
CTGGCCCTTTTCCAAGGGTGGTCAGCCTCAGAACCTTACTTGCACTGGAATAAAATCAGTGT  
CATAGGACAGACCATGTCCTGGACCTGGAGCTCCCTAACAAAGGCTGATTTATCAGGCAATGAGA  
TCGAAGCTTCAGTGGACCCAGTGTGTTCCAGTGTGTCCCAGTCTGAGCTGAGGTTAGCCAG  
TCCAACAAAGCTCACATTATGGTCAAGAGATTGGATTCTGGATATCCCTCAATGACATCAG  
TCTTGCTGGGAATATATGGGAATGCAAGCAGAAATATTGCTCCCTGTAAACTGGCTGAAAGTT  
TTAAAGGCTAAAGGAGAATACAATTATCTGCACTGCCCAGAGCTGCAAGGAGTAAATGTG  
ATCGATGCAAGAAACTACAGCATCTGGCAAAGTACTACAGAGAGGTTGATCTGGCAG  
GGCTCTCCAAAGCCGACGTTAACGCCAACGCTCCCCAGGCCAGACATGAGAGCAAACCCCTT  
TGCCCCCGCGTGGGAGGCCAACAGAGCCGCCAGAGACCGATGCTGACGCCGAGCACATCT  
TTCCATAAAATCATCGCGGGCAGCGTGGCGTTTCTGTCGTCATCCTGCTGGTTAT  
CTACGTTCATGGAAGCGGTACCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGGAA  
GGCACAGGAAAAGAAAAGACAGTCCCTAACGAAATGACTCCCAGCACCCAGGAATTATGTA  
GATTATAAAACCCACCAACCGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTA  
TAACAAATGGGCTCAGGGAGTGTGAGGTATGAACCTTGTGATAAAAAGAGCTTAAAGCT  
GGGAAATAAGTGGTCTTATTGAACTCTGTAAGTCAAGGGAACCGCGATGCCCTCCCC  
TTCCCTCTCCCTCACTTTGGCAAGATCCTCTGTCCGTTTAGTGCATTATAACT  
GGTCATTTCCTCTACATAATCAACCCATTGAAATTAAACACAAATCAATGTGAAGCTT  
GAACCTCCGGTTAATATAACCTATTGTATAAGACCCCTTACTGATTCCATTATGTCGCA  
GTTTAAGATAAAACTTCTTCATAGTAAAAAAAAAA

## **FIGURE 124**

MGFNVIRLLSGSAVALVIAPTVLITMLSSAERGCPKGCRCEGKMYCESQKLQEIPSSISAGCLG  
LSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLNNTR  
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHRSNSLRTIPVRIFQDCRNLELLDLGYNRIRS  
LARNVFAGMIRLKEHLHEHNQFSKLNLAFFPLVSLQNLQWNKISVIGQTMSTWSSLQRLDL  
SGNEIEAFSGPSVFQCVPNLQRNLDSNKLFIGQEILDWSISLNDISLAGNIWECSRNICSLVN  
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE  
SKPPLPPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLILLVIYVSWKRYPASMKQLQQR  
SLMRRHRKKKRQSLKQMTPSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

## **FIGURE 125**

CCGTTATCGTCTTGCCTACTGCTGAATGTCCGTCCCGGAGGAGGGAGGGCTTTGCCGCTG  
ACCCAGAGATGGCCCCGAGCGAGCAAATTCTACTGTCCGGCTGCGGGCTACCGTGGCGAGCT  
AGCAACCTTCCCCTGGATCTCACAAAACTCGACTCCAATGCAAGGAGAACGAGCTTGTCTC  
GGTGGGAGACGGTGCAAGAGAACTGCCCCTAGGGGAATGGTGCGCACAGCCCTAGGGATC  
ATTGAAGAGGAAGGCTTCTAAGCTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT  
GTATTCTGGAGGT~~CGA~~ATGGTCACATATGAACATCTCCGAGAGGTTGTGTTGGAAAGTGAAG  
ATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGGATGGCTGGTGTATTGGCCAGTT  
TTAGCCAATCCAACTGACCTAGTGAAGGTT~~CAGATG~~CAATGGAAGGAAAAGGAAACTGGAAGG  
AAAACCATTGCGATT~~CGTGGT~~GTACATCATGCATTGCAAAATCTTAGCTGAAGGAGGAATAC  
GAGGGCTTGGGCAGGGCTGGGTACCCAATATAACAAAGAGCAGCACTGGTGAATATGGGAGATT  
ATACCACTTATGATACAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA  
TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA  
TCAAAAGCAGAATAATGAATCAACCACGAGATAAACAGGAAGGGACTTTGTATAAATCATCG  
ACTGACTGCTTGATT~~CAGGCT~~GTTCAAGGT~~GAAGGATT~~CATGAGTCTATATAAAAGGCTTTTACC  
ATCTTGCTGAGAATGACCCCTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGA  
TGAGTGGAGTCAGTCCATTTAA

## **FIGURE 126**

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPPLDLTKTRIQLMQGEAALARLGDGARES  
APYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFGKSEDEHYPLWKS  
VIGGMMAGVIGQFLANPTDLVKVQMOMEGKRKLEGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP  
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCGLVASILGTPADVIKSRI MNQP  
RDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

## **FIGURE 127**

CGCGGATCGGACCCAAAGCAGGTGGCGGCCGGCAGGAGAGCAGGCCGGCGTCAGCTCTCGAC  
CCCCGTGTCGGGCTAGTCCAGCGAGGCAGGGCGCTGGGCCATGCCAGGCCGGCATGG  
AGCGGTGGCGCAGCCGGCTGGCGCTGGTGACGGGGCCTCGGGGGCATCGGCGCGCGTGGCC  
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGCTGCGCCCGACTGTGGCAACATCGAGGA  
GCTGGCTGCTGAATGTAAGAGTCAGGCTACCCCGGACTTGATCCCCTACAGATGTGACCTAT  
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGAGACATC  
TGCATCAACAATGCTGGCTGGCCGGCCTGACACCCTGCTCTCAGCAGCACCAGTGGTTGGAA  
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATTGACACAGGGCTACCAAGTCCATGA  
AGGAGCAGAATGTGGACGATGGCACATCATTAACATCAATAGCATGTCAGGCCACCGAGTGTAA  
CCCCCTGTCGTGACCCACTTCTATAGTGCACCAAGTATGCCGTCAGTGCCTGACAGAGGGACT  
GAGGCAAGAGCTCGGGAGGCCAGACCCACATCCGAGCCACGTGCATCTCCAGGTGTGGTGG  
AGACACAAATTGCGCTTCAAACCTCCACGACAAGGACCTGAGAAGGAGCTGCCACCTATGAGCAA  
ATGAAGTGTCTCAAACCGAGGATGTGGCCGAGGCTGTTATCTACGTCCAGCACCCCCGCACA  
CATCCAGATTGGAGACATCCAGATGAGGCCACGGAGCAGGTGACACTGTGACTGTGGGAGCTCC  
TCCTTCCTCCCCACCCCTCATGGCTGCCCTGCCTCTGGATTAGGTGTTGATTTCTGGAT  
CACGGGATAACCACTCCCTGTCCACACCCCGACCAGGGCTAGAAAATTGTTGAGATTTTATA  
TCATCTGTCAAATTGCTTCAGTTGAAATGTGAAAAATGGGCTGGGAAAGGAGGTGGTGTCCC  
TAATTGTTTACTTGTAACTTGTCTTGCCCTGGCACTTGGCTTGTCTGCTCTCAGTG  
TCTTCCCTTGACATGGGAAAGGAGTTGTGCCAAAATCCCCATCTTGCACCTCAACGCTG  
TGGCTCAGGGCTGGGTGGCAGAGGGAGGCCTCACCTTATATCTGTGTTATCCAGGGCTCC  
AGACTTCCCTCTGCCTGCCCACTGCACCCCTCCCCCTATCTATCTCCTCTCGGCTCCCC  
AGCCCAAGTCTGGCTTGTCCCCCTGGGTATCCCTCACTGACTCTGACTATGGCAG  
CAGAACACCAGGGCTGGCCAGTGGATTTCATGGTATCATTAAAAAGAAAATCGCAACCAA  
AAAAAAAAAA

## **FIGURE 128**

MARPGMERWRDRRLALVTGASGGIGAAVARALVQQGLKVVGCARTVGNIIEELAAECKSAGYPGTLLI  
PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVLALSICTR  
EAYQSMKERNVDDGHIININMSGHRLPLSVTHFYSATKYAVTALTEGLRQELREAQTHIRATC  
ISPGVVETQFAFKLHDKDPEKAAATYEQMCKLPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

## **FIGURE 129**

AACTTCTACATGGGCCTCCTGCTGGTGCTCTTCAGCCTCTGCCGGTGCCTACACCAT  
CATGTCCCTCCCACCCCTCTTGACTGCGGCCGTTCAAGGTGCAGAGTCTCAGTTGCCGGAGC  
ACCTCCCCCTCCCGAGGCAGTCTGCTCAGAGGGCTCGGCCAGAATTCCAGTTCTGGTTCATGC  
CAGCCTGTAAGGGCATGGAACTTGGTGAAATCACCGATGCCATTAAAGAGGGTTTCTGCCA  
GGATGGAAATGTTAGGTCGTTCTGTCTGCCTGTTCAATTTCAGTAGCCACCAGCCACCTGTGG  
CCGTTGAGTGCTGAAATGAGAACTGAGAAAATTAAATTCTCATGTATTTCTCATTTATTAA  
TTAATTAACTGATAGTTGTACATATTGGGGTACATGTGATAATTGGATACTGTATAACAA  
TATATAATGATCAAATCAGGGTAACGGGATATCCATCACATCAAACATTATTTTATTCTTT  
TTAGACAGAGTCTCACTGTCAACCAGGCTGGAGTGCAGTGGGCCATCTCAGCTTACTGCAAC  
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCACCTCCAAAGTAGCTGGGACTACAGGCAT  
GCACCACAATGCCCAACTAATTGTATTTAGAGACGGGGTTTGCCATGTTGCCAGG  
CTGGCCTGAACTCCTGGCCTCAAACAATCCACTGCCTCGGCCTCCCAAAGTGTATGATTACA  
GGCGTGAGCCACCGTGCCTGGCTAACATTTATCTTGTGTTGGAACTTGAAATTAT  
ACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGACTTCTCCCTCT  
ATCTAACTGTATATTGTACCAAGTTAACCAACCGTACTTCATCCCCACTCCTCTATCCTCCC  
AACCTCTGATCACCTCATTCTACTCTACCTCCATGAGATCCACTTTTAGCTCCCACATGTG  
AGTAAGAAAATGCAATATTGTCTTCTGTGCCTGGCTTAACTAACATAATGACTCCTG  
TTCCATCCATGTTGGCTGCAAATGACAGGATTCGTTCTTAATTCAATTAAAATAACCACACATG  
GCAAAAA

## **FIGURE 130**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSSLRGPRPRIPLVSCOPV  
KGHGTLGESPMPFKRVFCQDGTVRSFCVCAVFSSHQPPVAVECLK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 86-92

**Zinc carboxypeptidases, zinc-binding region 2 signature.**

amino acids 68-79

## **FIGURE 131**

TTCTGAAGTAACGGAAGCTACCTTGATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC  
ATCTTCCTCATCGGGACTAAAATTGGGCTTCTCAAGTAGCACCTCATCAGTTATGGCTAAATCCTG  
TCCATCTGTGTGCGCTGCGATGCGGTTTCATTACTGTAATGATCGTTCTGACATCCATTCAAACAG  
GAATACCAGAGGATGCTACAACCTCTACCTCAGAACACCAAATAAAATAATGCTGGGATTCCCTTCAGAT  
TTGAAAAAACTTGTGAAAGTAGAAAGAATATACTATACCAACACAGTTAGATGAATTTCCTACCAACCT  
CCCAGGAACTATGTAAGAGTTACATTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTCAA  
AAATTCCCTATCTGAAAGAATTACATTTAGATGACAACCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA  
TTCCGAGACAGCAACTATCTCGACTGCTTTCTGTCCCGTAATCACCTAGCACAATTCCCTGGGTTT  
GCCAGGACTATAGAAGAACTACGCTGGATGATAATCGCATATCCACTATTCATCACCCTCTTCAAG  
GTCTCACTAGTCTAAACGCCTGGTTAGATGAAACCTGTGAAACAATCATGGTTAGGTGACAAAGTT  
TTCTTCAACCTAGTTAATTGACAGAGCTGTCCTGGTGCAGAATTCCCTGACTGCTGCACAGTAAACCT  
TCCAGGCACAAACCTGAGGAAGCTTATCTCAAGATAACCACATCAATGGGTGCCCAATGCTTTT  
CTTATCTAAGGCAGCTCTACGACTGGATATGTCATAATAAACCTAAGTAATTACCTCAGGGTATCTT  
GATGATTGGACAATATAACACAACGTTCTCGCAACAATCCCTGGTATTGCGGGTGCAGATGAAATG  
GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTATGTGCCAAGCCCCAGAAA  
AGGTTCGTGGGATGGCTATTAGGATCTCAATGCAAGACTGTTGATTGTAAGGACAGTGGGATTGTAAGC  
ACCATTCAAGATAACCACGCAATAACCCACACAGTGTATCCTGCCAAGGACAGTGGCCAGCTCCAGTGAC  
CAAACAGCCAGATATTAAGAACCCCAAGCTCAACTAAGGATCAACAAACCAAGGGAGTCCCTCAAGAAAAAA  
CAATTACAATTACTGTGAAGTCTGTCACCTCTGATACCATTCTATCTTGGAAACTTGCTCTACCTATG  
ACTGCTTGGACTCAGCTGGCTTAAACTGGGCATAGCCGGCATTTGGATCTATAACAGAAACAATTGT  
AACAGGGGAACGCACTGAGTACTGGTCACAGCCCTGGAGCCTGATTCACCTATAAAGTATGCATGGTC  
CCATGGAAACCAGCAACCTCTACCTATTGATGAAACTCCTGTTGATTGAGACTGAAACTGCACCCCT  
CGAATGTACAACCCCTACAACCACCCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTAC  
TTGGCTGCCATATTGGTGGGCTGTGGCCCTGGTTACCATGGCTTCTGCTTAGTGTGTTGGTATG  
TTCATAGGAATGGATGCTCTTCTCAAGGAACGTGTGCAATAGCAAAGGGAGGAGAAGAAAGGATGACTAT  
GCAGAAGCTGGCACTAAGAAGGACAACACTATCCTGGAAATCAGGGAAACTTCTTTCAAGATGTTACCAAT  
AAGCAATGAACCCATCTGAAGGAGGAGTTGTAATACACACCATATTCTCTTAATGGAATGAATCTGT  
ACAAAAACAATCACAGTGAAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC  
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTGGTTTAAACCTAAGGGAGGTGATG  
GT

## **FIGURE 132**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRCDAAGFIYCNDRFLTSIPTGIPEDATTLYL  
QNNQINNAGIPSIDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKIPYL  
EELHLDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSIIPWGLPRTIEELRLDDNRISTISSPSL  
QGLTSLKRLVLDGNLLNNHGLGDVKFFNLVNLTELSVRNSLTAAPVNLPGTNLRKLYLQDNHIN  
RVPPNAFSYLRQLYRLDMSNNNLSNPQGIFDDLDNITQLILRNNPWYCGCKMKWVRDWLQSLPV  
KVNVRGILMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQGQWPAPVTKQPD  
IKNPKLTDQQTTGPSRKTITITVKSVTSDTIHISWKALPMTALRLSWLKLGHSPAFGSITET  
IVTGERSEYLVTALEPDSPYKVMVPMETSNLYLFDETPVCIETETAPLRMYNPTTLNREQEKE  
PYKNPNLPLAAIIGGAVALVTIALLAVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS  
ILEIRETSFQMLPISNEPISKEEFVIHTIFFPNGMNLYKNNHSESSSNRSYRDSGIPDSDHSHS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 531-552

**N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

**Tyrosine kinase phosphorylation site.**

amino acids 515-522

**N-myristoylation sites.**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,  
640-645

**Amidation site.**

amino acids 567-570

**Leucine zipper pattern.**

amino acids 159-180

**Phospholipase A2 aspartic acid active site.**

amino acids 34-44

### **FIGURE 133**

CCGTCATCCCCCTGCAGCCACCCCTCCCAGAGTCCTTGCCTGCCAGGCCACCCAGGCTTCTGGCA  
GCCCTGCCGGGCCACTTGTCTTCCATGTCTGCCAGGGGAGGTGGGAAGGAGGTGGAGGAGGGCG  
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGTGAGCGTGACCAGCAGTGAGCAGAG  
GCCGGCCATGGCCAGCCTGGGCTGCTGCTCTGCTTAAGTACGACAGCACTGCCACCGCTGTGGT  
CCTCTCACTGCCCTGGCTGGACACTGCTGAAAGTAAAGCCACCATGCAAGACCTGATCCTGTCT  
GCGCTGGAGAGAGCCACCGTCTCCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGATGGT  
GGGGTCCGAGTGTGGAAGAGCAGCTAAAAAGTGTCCGGAGAAGTGGGCCAGGAGCCCTGC  
TGCAGCCGCTGAGCTGCGCGTGGGATGCTGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC  
CTCCACTACCTCAAGCTGAGTGATCCAAAGTACCTAACAGAGAGTTCCAGCTGACCCTCCAGCCCG  
GTTTGGAAAGCTCCACATGCCCTGGATCCACACTGATGCCCTTGGTGTACCCACGTTGGC  
CCCAGGACTCATTCTCAGAGGAGAGAAGTGAAGTGCAGCTGCGCTGGTGCAGCTGCTGGAAACCGGACG  
GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCGGCTGCTC  
AGGCTACTGCCCTGCCCACCAACTGCTCTTCTCTGGCCAGAATGAGGGATGCACACAGG  
GACCACTCCAACAGAGCCAGGACTATATCAACCTTCTGCGCAACATGATGGACTTGAACCGC  
AGAGCTGAGGCCATCGGATAACGCCAACCTACCCGGACATCTTATGGAAAACATCATGTTCTG  
TGGAAATGGGCGCTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA  
AACAGCAGGAAGGATGCTCGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA  
TATCAGCAGCATTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTCCAGATTCTCGCTCTGT  
TGCTCAGGCTGGAGTACAGTGGCGCAATCTGGCTCACTGCAACCTTGCCTCTGGGTTCAAGC  
AATTCTCTGCCCTCATCCTCCCGAGTAGCTGGACTACAGGAGCGTGCCACCACCTGGCTAAT  
TTTATATTTTTAGTAGAGACAGGGTTCATCATGTTGCTCATGCTGGTCTCGAACCTCTGAT  
CTCAAGAGATCCGCCACCTCAGGCTCCAAAGTGTGGATTTAGGTGTGAGCCACCGTGTCTG  
GCTGAAAAGCATTCAAAGAGACTGTGTTGAATAAAGGGCAAGGTTCTGCCACCCAGCACTC  
ATGGGGCTCTCTCCCTAGATGGCTGCTCTCCACAAACACAGCCACAGCAGTGGCAGCCCTGG  
GTGGCTCTATACATCCTGGCAGAACACCCCCCAGCAAACAGAGAGGCCACACCCATCCACACCG  
CCACCAAGCAGCGCTGAGACGGACGGTCCATGCCAGCTGCCAGGAGGAACAGACCC  
TTAGTCCTCATCCCTAGATCCTGGAGGGCACGGATCACATCCTGGAAAGAAGGCATCTGGAGG  
ATAAGCAAAGCCACCCGACACCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG  
GGCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTCAACTGCAACTGAAAAAAAAAAA

## **FIGURE 134**

MSARGRWEGGGRRACRGSGLARAQGAERVTSSEQRPMASLGLLLLLLTALPPLWSSLPGLD  
TAESKATIADLILSALERATVFLQRLPEINLDGMGVVRVLEEQLKSVREKWAQEPLLQPLSLRV  
GMLGEKLEAAIQRSILHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE  
RSDVCLVQLLGTGTDSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQQSQD  
YINLFCANMMDLNRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILSWQKQQEGCFG  
EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNL GSLQPLPPGFQFSCLILP  
SSWDYRSVPYLANFYIFLVETGFHHVAHAGLELLISRDPPTSGSQSVGL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 39-56

**Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

**N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

**Amidation site.**

amino acids 10-14

**Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

### **FIGURE 135**

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTCCCGTCTGCTGCTG  
CTGCTGCTATCGGGGGATGTCCAGAGCTGGAGGTGCCCGGGCTGCTGCTGAGGGATCGGGAGG  
GAGTGGGGTCGGCATAGGAGATCGCTCAAGATTGAGGGCGTGCAGTTGTTCCAGGGGTGAAGC  
CTCAGGACTGGATCTGGCGGCCGAGTGTGGTAGACGGAGAAGAGCACGTCGGTTCTTAAG  
ACAGATGGGAGTTGTGGTTCATGATATACTTCTGGATTTATGTAGTGGAAAGTTGTATCTCC  
AGCTTACAGATTGATCCC GTT CGAGTGGATATCACTTCGAAAGGAAAATGAGAGCAAGATATG  
TGAATTACATCAAAACATCAGAGGTTGTCAACTGCCCTATCCTCTCAAATGAAATCTCAGGT  
CCACCTTCTTACTTTATTAAAAGGGAAATCGTGGGGCTGGACAGACTTCTAAATGAACCCAATGGT  
TATGATGATGGTCTTCCTTATTGATATTGTGCTCTGCCTAAAGTGGTCAACACAAGTGATC  
CTGACATGAGACGGAAATGGAGCAGTCATGAATATGCTGAATTCCAACCAGTTGCCTGAT  
GTTTCTGAGTTCATGACAAGACTCTCTCTCAAATCATCTGGCAAATCTAGCAGCGGCAGCAG  
TAAAACAGGCAAAAGTGGGCTGGAAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTGCAC  
AAACACGGCAACACTGGGTGGCATCCAAGTCTGGAAAACCGTGTGAAGCAACTACTATAAAACTT  
GAGTCATCCCGACGTTGATCTTACAACGTGTATGTT  
AACTTTTAGCACATGTTTGACTTGGTACACGAGAAAACCCAGCTTCATCTTGCTGTAT  
GAGGTCAATATTGATGTCACTGAATTAAATTACAGTGTCTATAGAAAATGCCATTAATAAAATTAT  
ATGAACTACTATAACATTATGTATTAATTAATTAACATCTTAATCCAGAAATCAAAAAAAA  
AAAAAAAAAAAAAAA

## **FIGURE 136**

MAAALWGFFPVLLLLLSDVQSSSEVPGAAEGSGGSGVGIGDRFKIEGRAVPGVKPQDWISAA  
RVLVDGEEHVGFLLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRARYVNYYIKTSE  
VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMLPPLLIFVLLPKVVNTSDPDMRREME  
QSMMNLNSNHELPDVSEFMTRLFSSKSSGKSSGSSKTGKSGAGKRR

**Important features of the protein:**

**Signal sequence:**

amino acids 1-23

**Transmembrane domain:**

amino acids 161-182

**N-glycosylation site.**

amino acids 184-187

**Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

**N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

**Amidation site.**

amino acids 238-241

**ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236

## **FIGURE 137**

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGA  
CCAGAAGGGTGAGCTACGTTGGCTTCTGGAAGGGGAGGCTATATGGTCAATTCCCCAAACAA  
GTTTGACATTCCCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC  
CTTACCTGCTGGCACTAACGGCGAGCCAGGATGGGACAGAATAAAGGAGCCACGACCTGTGC  
CACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTCTTCACGGGAGGCTTGGCAGT  
TTTCTTAACCTCTGTGGCTCCAGATTCAGGCCTAAGATGAAAGCCTTAGTCTTGCTTCAGC  
CTTCTCTGCTGCCCTTATCTCCTATGGACTCCTCACTGGACTGAAGACACTCAATTGGG  
AAGCTGTGTGATGCCACAAACCTCAGGAAATACGAAATGGATTCTGAGATAACGGGCAGTG  
TGCAAGCCAAGATGAAACATTGACATCAGAATCTAAGGAGGACTGAGTCTTGCAAGACACA  
AAGCCTGCGAATCGATGCTGCCCTGCCATTGCTAAAGACTCTATCTGGACAGGGTATTAA  
AAACTACCAGACCCCTGACCATTATACTCTCCGGAAAGATCAGCAGCCTGCCAATTCTTCTTA  
CCATCAAGAAGGACCTCCGGCTCTCATGCCACATGACATGCCATTGTGGGAGGAAGCAATG  
AAGAAATACAGCCAGATTCTGAGTCACTTGAAAAGCTGGAACCTCAGGCAGCAGTGTGAAGGC  
TTTGGGGAACTAGACATTCTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGTGATGCTG  
CTGCTAAGAATATTGAGGTCAAGAGCTCCAGTCTTCATAACCTGCAAGAGGAGCATGACCCAA  
ACCACCATCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTG  
CTTCCTGCTGATGTTGCTTATGCATCCCCAATCTAATTGAGACCATACTGTATAAGATTT  
TGTAATATCTTCTGCTATTGGATATATTATTAGTTAATATATTATTTATTTGCTATTAA  
ATGTATTATTTTACTTGGACATGAAACTTAAAAAAATTCACAGATTATTTATAACCTG  
ACTAGAGCAGGTGATGTATTATACAGTAAAAAAAAACCTGTAAATTCTAGAAGAGTGG  
CTAGGGGGTTATTCAACTAAGGACATATTACTCATGCTGATGCTGTGAGAT  
ATTGAAATTGAACCAATGACTACTTAGGATGGGTTGGAATAAGTTGATGTGGAATTGCAC  
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATATTGTATCTCAG  
CCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAGTTCTTGATACCAAAAAAAA  
AAAAAAAAAAA

## **FIGURE 138**

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRPEIF  
SSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG  
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLRHLLRLYLDRVFKNYQTPDHYTLRKIS  
SLANSFLTIKKDLRLSHAHMTCHCCEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET  
E

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

## **FIGURE 139**

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCAGGTGGGGTCGGTCCGCATCCAGCC  
TAGCGTGTCCACGATCGGCTGGGTCGGGACTTCTGCTACCTGTGCGTAGCGATCGAGGTGC  
TAGGGATCGGGCTTCCTCGGGATTCTCCCGCTCCGTTCTGCCTCTGCCAGAGCGGAA  
CACGGAGCGGAGCCCCAGCGCCGAACCTCGGCTGGAGCCAGTTCAACTGGACCACGCTGCC  
ACCACCTCTTCAGTAAAGTTTATGTCTGATAGATGCCTTGAGAGATGATTTGTGTTG  
GGTCAAAGGGTGTGAAATTATGCCCTACACAACCTTACGGAAAAGGAGCATCTCACAGT  
TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCCTGAATCAAGGCATTGATGACGGGGAG  
CCTTCCTGGCTTGTGACGTATCAGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGA  
TAAGACAAGCAAAGCAGCTGGAAAAGAAATAGTCTTTATGGAGATGAAACCTGGGTTAAATTA  
TTCCCAAAGCATTGTGAAATGATGGAACACCTCATTTCTGTGTCAGATTACACAGAGGT  
GGATAATAATGTCACGAGGCATTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAATCC  
TCCACTACCTGGGCTGGACCACATTGGCACATTCCAGGGCCAACAGCCCCCTGATTGGGAG  
AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCACTGAGTCGAAGGAGAGA  
GACGCCCTAACCAATTGCTGTTCTTGCTGACCATGGCATGTCAGAACAGGAAGTCACG  
GGGCCTCCCTCACCGAGGAGGTGAATACACCTCTGATTAAATCAGTCTGCGTTGAAAGGAAA  
CCCGGTGATATCCGACATCCAAGCAGTCCAATAGACGGATGTGGCTGCGACACTGGCGATAGC  
ACTTGGCTTACCGATTCCAAGAACAGTGTAGGGAGCCTCTATTCCAGTTGTTGGAAGGAAGAC  
CAATGAGAGAGCAGTGTGAGATTACATTGAATACAGTGCAGCTAGTAAACTGTTGCAAGAG  
AATGTGCCGTCATATGAAAAGATCCTGGGTTGAGCAGTTAAATGTCAGAAAGATTGCATGG  
GAACCTGGATCAGACTGTACTTGGAGGAAAGCATTCAAGTCTCTATTCAACCTGGGCTCCAAGG  
TTCTCAGGCACTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCAG  
TTCTCACCTGCTCTGCTCAGCTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCA  
CTGTCATCTCCTGGGTTCTCTGCTCTTATTGGTGTACCTGGGCTCTCGTGGCTGGCGAGGCT  
CAATTGTGTCACCTCAGCTGAAAGTCTGCTACTTGTGGCTCTGCAAGTGTGGCTGGCAGTGC  
GCCCTTCGTTTACCAAGACTCTGGTTGAAACACCTGGTGTGCAAGTGTGGCTGGCAGTGC  
AGGGGCTCAGGGAGGACGTTGAGCAGCCTTATCCAGGCCTGGGTGTCCGACACAGGTG  
TTCACATCTGTGCTGAGGTCAAGATGCCCTAGTTCTGGAAAGCTAGGTTCTGCGACTGTAC  
CAAGGTGATTGTAAGAGCTGGGGTCACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGAA  
TCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCACTGAGCTGAGGGAAAGAGACAAATGGCCTGGA  
CACTCAGGAGGGTCAAAAGGAGACTTGGTGCACCACTCATCCTGCCACCCCCAGAATGCATCCT  
GCCTCATCAGGTCCAGATTCTCAAGGGGACGTTCTGTAATTCTAGTCCTGGCC  
TCGGACACCTTCATTGTTAGCTGGGAGTGGTGGTGAGGCAGTGAAGAAGAGGGGGATGGTCAC  
ACTCAGATCCACAGAGCCCAGGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTGGGCCCC  
ACCCCAACCCCTGCACAGCCCTCATCCCTCTGGCTGAGCCGTCAAGAGGCCCTGTGCTGAGTGT  
CTGACCGAGACACTCACAGCTTGTCACTAGGGCACAGGCTTCCCTGGAGCCAGGATGATCTGTG  
CCACGCTTGCACCTGGGCCATCTGGCTCATGCTCTCTCTGCTATTGAATTAGTACCTAG  
CTGCACACAGTATGTAGTTACCAAAAGAATAACGGCAATAATTGAGAAAAAAA

## **FIGURE 140**

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTLLPPPLF  
SKVVIVILIDALRDDFVFGSKGVKFMPYTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF  
VDVIRNLNSPALLEDSVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTFFFSDYTEVDNNV  
TRHLDKVLKRGDWDLILHLHYLGLDHIGHISGPNSPLIGQKLSEMDSVLMKIHTSLQSKERETPLP  
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 58-76

**N-glycosylation sites.**

amino acids 56-60, 194-198

**N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

**Amidation site.**

amino acids 154-158

**Cell attachment sequence.**

amino acids 205-208

## **FIGURE 141**

GGCACGAGGAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCAGAGCTACTGCCCTACA  
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAACT  
TCCCTATAGAAAACAACTGCCAGCACCTTAAGACCACTACACACCTCAGAGTGAAGAACTTAAC  
CCGAAGAAATTCAGCATTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT  
AGCAGTTCCAGATAAAAACTACATCGCCCAGAGATCTTGCATTAGCCTCATCCTGAGCT  
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGTCTCAAAGGGAGTTGTCTAC  
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAAACTGATGAAGCT  
GGCTGCCAAAAGGAATCAGCACGCCGGCCCTTCATCTTGTAGGGCTCAGGTGGCTCCTGGA  
ACATGCTGGAGTCGGCGCTCACCCGGATGGTCATCTGCACCTCCTGCAATTGTAATGACCT  
GTTGGGGTGACAGATAAAATTGAGAACAGGAAACACATTGAATTTCAACCAGTTGCAA  
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAAACTGCCCAATTGAACGCCTTCTCGCTA  
ATTGAACTAATTGTATAAAAACCAAAACCTGCTCACT

## **FIGURE 142**

MLLLLLEYNFPIENNQHLKTTHTFRVKNLNPKKFSIHQDHKVLVLDGNLIAVPDKNYIRPEI  
FFALASSLSSASAEGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFI  
FYRAQVGWSNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 33-36

**N-myristoylation site.**  
amino acids 50-55, 87-92

**Interleukin-1**  
amino acids 37-182

### **FIGURE 14.3**

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTAA  
TCCAGGATCCTGTCTTCTGTCTGTAGGAGTGCCTGTTGCCAGTGTGGGTGAGACAAGTTG  
TCCCACAGGGCTGTCGAGCAGATAAGGATAAGGGCTGGGTCTGTGCTCAATTAACTCCTGTGGG  
CACGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGCCTGCCGTGG  
AAGGGAGGTCTGTCTGGCGCTGCTGCTGTTCTCTTAGGCTCCCAGATCCTGCTGATCTATGC  
CTGGCATTCCACGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA  
CAGTGGAGTTGCTGCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG  
CACATCTTGAATTCTGGAAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT  
GGGGAGAACTAGGTGTGGAAATTGAAGACGACATTGACAACGCCATTCCAAGAAAGCACAG  
AGCTGAACAATACTTACCTGCTTCTTCACCACAGCACCAGGCCCTGGATGACTCAGTTCAGC  
CTCCTGAACAAGACCTGCTGGAGGGATTCCACTGAGTGAAACCCACTCACAGGCTGTCCATGT  
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTCAGTGGCTGAGCAGCT  
TTGGACTTGTGTTATCCTATTTGATGTGTTGAGATCTCAGATCAGTGTGTTAGAAAATCC  
ACACATCTTGAGCCTAATCATGTAGTAGCATTAACATCAGCATTAAAGAAAAAAA  
AAA

## **FIGURE 144**

MLGLPWKGGLSWALLLLLLGSQILLIYAWHFHEQRDCDEHNMARYLPATVEFAVHTFNQQSKDY  
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQUESTELNNFTCFFTISTRP  
WMTQFSLLNKTCLEGFH

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 117-121, 139-143

**N-myristoylation site.**

amino acids 9-15

## **FIGURE 145**

CTGTGCAGCTGAGGCTCCAGAGGCACACTCCAGAGAGGCCAAGGTTCTGACGCG**AATGAGGAAG**  
CACCTGAGCTGGTGGCTGGCACTGTCTGCATGCTGCTCTCAGCCACCTCTGCGGTCCA  
GACGAGGGGCATCAAGCACAGAACAACTCAAGTGGAACCGGAAGGCCCTGCCAGCAGCTGCCAGATCA  
CTGAGGCCAGGTGGCTGAGAACCGCCGGAGCCTCATCAAGCAAGGCCAGCAGCTGACATT  
GACTTCGGAGCCGAGGGCAACAGGTACTACCGAGGCCAACTACTGGCAGTTCCCAGTGGCATCCA  
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTGTCAACGGCTGCATCAATGCCA  
CCCAGGGCGAACCAAGGGGGAGTTCCAGAACAGCAGAACAAAGCTCCACCAGCAGGTGCTCTGG  
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTGTTGGAGAGGGCGCAGGACT  
TCGGGTACCATGCACCAAGCCAGTGCTCCTGCCTCTGGCTTGATCTGGCTCATGGT**GAAAT**  
**AAGCTTGC**CAGGAGGCTGGCAGTACAGAGGCCAGCAGCAGCAAATCCTGGCAAGTGACCCAGCT  
CTTCTCCCCAAACCCACGCGTGTCTGAAGGTGCCAGGAGCGGCATGCACTCGCACTGCAA  
TGCGCTCCCACTGATGCGCCCTGGTATGTGCCTCGCTCTGATAGATGGGGACTGTGGCTTCT  
CCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGATAATGCTTGAT  
GAGAAGAACACATCAGGCAGTGCGCCACCTGCTTCACAGTACTTCCAACAACTCTAGAGGTAG  
GTGTATTCCGTTTACAGATAAGGAAACTGAGGCCAGAGAGCTGAAGTACTGCACCCAGCATC  
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCCTGGTTGTCTAACCCAGGTTTCTGCTCT  
GTCCAATTCCAGAGCTGTCTGGTGAATCACTTATGTCTCACAGGGACCCACATCAAACATGTAT  
CTCTAAATGAAATTGTGAAAGCTCCATGTTAGAAATAATGAAAACACCTGA

## **FIGURE 146**

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKOGRK  
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNLHQQ  
VLWRLVQELCSLKHCFFWLERGAGLRTMHQPVLLCLLALIWLVMVK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 157-171

**N-glycosylation sites.**

amino acids 98-102, 110-114

**Tyrosine kinase phosphorylation site.**

amino acids 76-83

**N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

**Amidation site.**

amino acids 62-66

## **FIGURE 147**

GCCTTGGCCTCCAAAGGGCTGGGATTATAGCGTGACCAACATGTCGGTCCAGAGTCTCATTT  
CCTGATGATTTATAGACTCAAAGAAAACTCATGTTCAGAAGCTCTCTCTGGCCTCCCT  
CTGTCTTCTTCCCTTTCTTCTTATTAAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG  
AAATCTTCATTTGCTTGTCAAGTGGGTAGGTCACTGAGTCTTAGTTTTATTGGAAATTT  
CAACTTCAGATTCAAGGGGTACATGTGAAGGTTGTTTATGAGTATATTGCATGATGCTGAGG  
TTTGGGGT

## **FIGURE 148**

MFRSSLLFWPPLCLLSLFLLLILISSIYSESCKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE  
GLFYEYIA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-myristoylation site.**

amino acids 62-68

## **FIGURE 149**

GTCTCCGCGTCACAGGAACCTCAGCACCCACAGGGCGGACAGCGCTCCCTCTACCTGGAGACTTGAC  
TCCC CGCGCCCCAACCTGCTTATCCCTGACCGTCGAGTGTCAAGAGATCCTGCAGCCGCCAGTCC  
CGGCCCCCTCTCCCGCCCCACACCCACCCCTCTGGCTTTCTCTGTTTACTCCTCCTTTCATTATA  
ACAAAAGCTACAGCTCCAGGAGCCAGCGGGGCTGTGACCCAAGCCAGCGTGGAAAGAATGGGTT  
CCTCGGGACCGGCACCTGGATTCTGGTGTAGTGCTCCGATTCAAGCTTCCCCAACCTGGAGGAA  
GCCAAGACAAATCTCTACATAATAGAGAATTAAAGTGCAGAAAGACCTTGAATGAACAGATTGCTGAA  
GCAGAAGAAGACAAGATTAAAAAAACATATCCTCCAGAAAACAAGCCAGGTCAAGAGCAACTATTCTT  
TGTGATAACCTGAACTGCTAAAGGAATAACAGAAAAGAAAAATTGAGAAAGAAAGACAATCTA  
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAAGATGTTGATTCAACCAAGAAATCGAAAATG  
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTCAAGATGATCCAGATGGTCTCA  
TCAACTAGACGGGACTCCTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTATGAAG  
AAAATGACAGAGCCGTGTTGACAAGATTGTTCTAAACTACTTAATCTGGCCTTATCACAGAAAGC  
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTACAAAATTAATCTCAAAGGAAGCCAACAA  
TTATGAGGAGGATCCAATAAGCCCACAAGCTGGACTGAGAAATCAGGCTGGAAAATACCAAGAGAAAG  
TGACTCCAATGGCAGCAATTCAAGATGGTCTGCTAAGGGAGAAACGATGAAACAGTATCTAACACA  
TTAACCTGACAAATGGCTTGGAAAGGAGAAACTAAAACCTACAGTGAAGACAACCTTGAGGAACCTCA  
ATATTCCTAAATTCTATGCGCTACTGAAAAGTATTGATTCAAGAAAAGAAGCAAAGAGAAAGAAA  
CACTGATTACTATCATGAAAACACTGATTGACTTGTGAAGATGATGGTGAATATGGAACAATATCT  
CCAGAAGAAGGTGTTCTACCTGAAAACCTGGATGAAATGATTGCTCTCAGACCAAAACAAGCT  
AGAAAAAAATGCTACTGACAATATAAGCAAGTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAA  
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAA  
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAACAGAAGCCTATTTGGAAGC  
CATCAGAAAAAAATATTGAATGGTGAAGAAACATGACAAAAGGAAATAAGAAGATTATGACCTT  
CAAAGATGAGAGACTTCATCAATAAACAAAGCTGATGTTATGTGGAGAAAGGCATCCTTGACAAGGAA  
GAAGCCGAGGCCATCAAGCGCATTATAGCAGCCTGTAAAATGGCAAAGATCCAGGAGTCTTCAA  
CTGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAAATTTTGACCCAAGG  
GTTATTAGAAAAGTGTGAATTACAGTAGTTAACCTTTACAAGTGGTTAAAACATAGCTTCTTCCC  
GTAAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAA

## **FIGURE 150**

MGFLGTGTWILVLVLPQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG  
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK  
FQDDPDGLHQLDGTPPLTAEDIVHKIAARIYEENDRAVFDFKIVSKLLNLGLITESQAHTLEDEVAE  
VLQKLISKEANNYEEDPNKPPTSWTENQAGKIKEVKTPMAAIQDGLAKGENDETVSNTLTLTNGLE  
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV  
SYLENLDEMIALQTKNKLEKNATDNISKLFPAPSEKSHEETDSTKEAAKMEKEYGSLKDSTKDD  
NSNPGGKTDEPKGTEAYLEAIRKNIEWLKKHDKGKGNKEDYDLSKMRDFINKQADAYVEKGILDK  
EEAEAIIKRIYSSL

**N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

**Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

**N-myristoylation sites:**

amino acids 143-148, 239-244

## **FIGURE 151**

CGGCTCGAGGCTCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCGTGGAGCTCAA  
GATGGCTCTGACTGGGGCCTGTGCTTCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC  
ATAATAACCACTCTAGCTGGAGGGCTGCATGCAGGGAAAGGTCAATTAAAGGTGAAGAGATCAGC  
GTGGTCCCCATGGTGGCTGGATGCCAGCTGTCCCCCTCATCCTGGGTGTCAGGGTGGAAAG  
CCAGTGCTGTCATGTGGGTGGGCAGGAGCCACTAACAAGTAGAGCCAGTGAACATCATGG  
AGCTCTATCTGGTCCAAGGAATCCAAGAGCTTCACCTCTACCAGGGGACATGGGGCTCACC  
TCCAGCTCGAGTCGGCTGCCTACCCGGCTGGTCTGTGCACGGCTGAAGCCGATCAGCC  
TGTCAAGACTCACCCAGCTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACTCC  
AGCAGTGTGACTAGGGCAACGTCCCCCAGAACCTCCCTGGGAGAGCCAGCTGGGTGAGGGT  
GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTGCTCAGGACCCCACGTCTGACTTAG  
TGGGCACCTGACCACTTGTCTCTGGTCCAGTTGGATAAAATTCTGAGATTGGAGCTCAGT  
CCACGGCTCTCCCCACTGGATGGTACTGCTGTGAAACCTTGTAAAAACCATGTGGGTAAA  
CTGGGAATAACATGAAAAGATTCTGTGGGGTGGGGAGTGGTGGGAATCATTCTGCT  
TAATGGTAAGTGTACCTGAGCCCCGAGGCCAACCCATCCCCAGTGTGAGCCTTATA  
GGGTCAAGTAGCTCCACATGAAGTCTGTCACTCACCACTGTGCAGGAGAGGGAGGTGGTCATA  
GAGTCAGGGATCTATGGCCCTGGCCCAGCCCCACCCCCCTTAACTCTGCCACTGTCTATA  
TGCTACCTTCTCTATCTCTCCCTCATCATCTTGTGGCATGAGGAGGTGGTGTGAGAA  
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCTCTTTAAAAACCAA  
GATAACAATCAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAGTGTCTGACATATTGAGA  
AGACCTACTTACAAGTGGCATATATTGCAATTATTAAATTAAAGATAACCTATTATATT  
TCTTTATAGAAAAAGTCTGGAAGAGTTACTTCATTTGCAATTGTAGCAATGTCAGGGTGGCAGT  
AGGTGATTTCTTTAATTCTGTTAATTATCTGTTCTCTTAATTCTACAAATGAAGATGA  
ATTCTTGTATAAAAATAAGAAAAGAAATTAAATCTTGTGAGGTTCTCTTAATTCTACAAATGAAGATGA  
TTGCTCTCAGCCTCCACTTCCCAGAGTAATTCAAATTGAAATGAGCTCTGCTGCTCTGGTTGG  
TTGTTAGTAGTGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGGCTGTGCTGAGTTGT  
GTGGCTGGAATCTGGGTAGGAACCTTAAAGAACAAAATCATCTGGTAATTCTTCTAGAAG  
GATCACAGCCCCGGATTCCAAGGCATTGGATCCAGTCTAAGAAGGCTGCTGACTGGTGA  
ATTGTGCCCCCTCAAATTCACATCTTCTGGAATCTCAGTGTGAGTTATTGGAGATAAG  
GTCTCTGAGATGTAGTTAGTTAAGACAAGGTATGCTGGATGAAGGTAGACCTAAATTCAATAT  
GACTGGTTCTGTATGAAAAGGAGGGACACAGAGACAGAGGAGACGCCGGGAAGACTATGTA  
AAGATGAAGGCAGAGATCGGAGTTTGCAAGGCCACAAGCTAAGAAACCCAAGGATTGGCAACC  
ATCAGAAAGCTTGGAGAGGCAAAGAAGAATTCTCCCTAGAGGCTTAGAGGGATAACGGCTCTG  
CTGAAACCTTAATCTCAGACTTCCAGCCTCTGAACGAAGAAAGAATAATTGGCTTTAA  
GCCACCAAGGATAATTGGTACAGCAGCTCTAGGAAACTAATACAGTGTCTAAATGATCCCTGT  
CTCCTCGTGTTCATTCTGTGTGTCCTCCCACAATGTACCAAGTTGTCTTGTGACCAA  
TAGAATATGGCAGAAGTGTGATGGCATGCCACTTCAAGATTAGGTTATAAAAGACACTGCAGCTTC  
TACTTGAGCCCTCTCTCTGCCACCCACGGCCCCAATCTATCTGGCTACTCGCTCTGGGG  
AAGCTAGCTGCCATGCTATGAGCAGGCTATAAGAGACTTACGTGTTAAAAAGTGAAGTCTCCT  
GCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATTTGTTTT  
AAGTTGCTCAGTTGGTCAACTTGTATGCAGCAATAGATAAATAATGCAAGAGAAAGAG

## **FIGURE 152**

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEIISVVPNRWLDASLSPVILGVQGGS  
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP  
VRLTQLPENGGWNAPITDFYFQQCD

**N-myristoylation sites.**

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

**Interleukin-1 signature.**

amino acids 111-131

**Interleukin-1 proteins.**

amino acids 8-29, 83-120, 95-134, 64-103

### **FIGURE 153**

CTTCAGAACAGGTTCTCCTCCCCAGTCACCAGTGCTCGAGTTAGAATTGTCTGCAATGGCCGC  
CCTGCAGAAATCTGTGAGCTTTCCCTATGGGGACCCCTGGCCACCAGCTGCCTCCCTCTGG  
CCCTCTGGTACAGGGAGGAGCAGCTGCGCCCCATCAGCTCCCACTGCAGGCTTAGCAGTCAAAC  
TTCCAGCAGCCTATATCACCAACCGCACCTCATGCTGGCTAAGGAGGCTAGCTGGCTGATAA  
CAACACAGCAGTCCGCTCATTGGGAGAAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT  
ATCTGATGAAGCAGGTGCTGAACTTCACCCTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTC  
CAGCCTTATATGCAGGAGGTGGTGCCCCTTCCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA  
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAGCTGAAGGACACAGTGAAAAGC  
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTGCTGTTATGCTCTGAGAAAT  
GCCTGCATTTGACCAGAGCAAAGCTGAAAATGAATAACTAACCCCTTCCCTGCTAGAAATAA  
CAATTAGATGCCCAAAGCGATTTTTAACCAAAAGGAAGATGGAGCCAAACTCCATCATG  
ATGGGTGGATTCCAAATGAACCCCTGC GTTAGTTACAAGGAAACCAATGCCACTTTGTTATA  
AGACCAGAAGGTAGACTTCTAACGCATAGATATTGATAACATTCAATTGTAACTGGTGTTC  
TATACACAGAAAACAATTTATTAAATAATTGTCTTTCCATAAAAAAGATTACTTTCCAT  
TCCTTAGGGAAAAAAACCCCTAAATAGCTCATGTTCCATAATCAGTACTTTATATTATAAA  
TGTATTTATTATTATAAGACTGCATTTATTTATCATTATTAATATGGATTATTAT  
AGAAACATCATTGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTATGACAATAATTAT  
AGAGCTTATAACATGTTATTGACCTCAATAAACACTTGGATATCCC

## **FIGURE 154**

MAALQKS VSSFLMGT LATSCLLL ALLVQGGAA APISSH CRLDKS NFQQPY ITNRT FMLAKEASL  
ADNNNTDV RLIGEKL FHGVSM SERCYLMK QVILNFT LEEVLFPQS DRFQP YMQEV VPFLARLSNRLS  
TCHIEGDDLHIQRNVQKLKD TVKKLGE SGEIKAIGEL DLLFMSLRNACI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

**N-myristoylation sites.**

amino acids 14-20, 82-88

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21

## **FIGURE 155**

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT  
CAGTCAGTGCCCGACTTGTGACTGAGTGTGCAGTGCCCAGCATGTACCAGGTCACTGCAGAGGGC  
TGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC  
TGCCAGGTTGGGCTGGGGCCAAGTGGAGTGAAGAAACTGGATCCAGGGGAGGGTGCAGAT  
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCATTAGCCTTTCCACAGGTGGTTGCAT  
TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCAGCTGCTGCCAGCAAAGGG  
CAGGACACCTCTGAGGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCTAGAGCCTGCTAG  
GCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTAACAGCAGGGCCATCT  
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGACCTGTACACGCCGT  
TGCCTGTGCCCGACTCGTCAGCCTACAGACAGGCTCCCACATGGACCCCGGGCAACTCGGA  
GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCCACA  
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTGTGTGTGCAGGGCCGT  
GTGATGGGCTAGCGGACCTGCTGGAGGCTGGTCCCTTTGGAAACCTGGAGCCAGGTGTACA  
ACCACTTGCCATGAAGGGCAGGATGCCAGATGCTTGCCTGTGAAGTGTCTGGAGCAG  
CAGGATCCGGGACAGGATGGGGCTTGGAAAACCTGCACTTCTGCACATTTGAAAAGAG  
CAGCTGCTGCTTAGGGCCGCCGAAGCTGGTGTCTGTCACTTCTCAGGAAAGGTTTCAA  
GTTCTGCCCTTCTGGAGGCCACCACTCCTGTCTTCCCTTTCCATCCCTGCTACCCCTG  
GCCCAAGCACAGGCACCTCTAGATAATTCCCCCTGCTGGAGAAGAAAGGCCCTGGTTTATT  
TGTTTGTGTTACTCATCACTCAGTGAGCATCTACTTGGGTGCATTCTAGTGTAGTTACTAGTCTT  
TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTATCAAATAAATAT  
CTTTATTAATAAATGAAAAAA

## **FIGURE 156**

MRERPRILGEDSSLISLFLQVVAFLAMVMGTHTYSHWPSCCPSPKGQDTSEELLRWSTVPVPPLEPA  
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS  
ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-32

**N-glycosylation site.**

amino acids 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 127-135

**N-myristoylation sites.**

amino acids 44-50, 150-156

## **FIGURE 157**

CCGGCG**A**TGTCGCTCGTGCTGCTAAGCCTGGCCGCGTGTGCAGGAGCGCCGTACCCCGAGAGCC  
GACC**G**TTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAACCC  
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTGCAACAGGGGACTATTCA  
ATTTGATGAATGTAAGCTGGGACTCCGGCAGATGCCAGCATCCGTTGTTGAAGGCCACCAA  
GATTGAGTGTGACGGCAAAAGCAACTTCCAGTCCTACAGCTGTGAGGTGCAATTACACAGAGG  
CCTTCCAGACTCAGACCAGACCCCTGGTGGTAAATGGACATTTCTACATCGGCTTCCCTGTA  
GAGCTGAACACAGTCTATTTCATTGGGCCATAATTCCTAATGCAAATATGAATGAAGATGG  
CCCTTCATGTCTGTGAATTTCACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAAA  
AGTGTGTCAAGGCCGAAGCCTGTGGGATCGAACATCACTGTTGTAAGAAGAATGAGGAGACA  
GTTAGAAGTGAACCTCACACCCTCCCCTGGGAAACAGATACTGGCTTATCCAACACAGCAC  
TATCATCGGGTTTCTCAGGTGTTGAGCCACACCAGAAGAAACAAACGCGAGCCTCAGTGGTGA  
TTCCAGTGACTGGGAGATGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTCCTACTTGTGGC  
AGCGACTGCATCCGACATAAGAACAGTTGTGCTCTGCCACAAACAGGCCTTCCCT  
GGATAACAAACAAAAGCAAGCCGGAGGCTGGCTGCCTCTCCTCTGCTGTCTGCTGGTGGCA  
CATGGGTGCTGGTGCAGGGATCTATCTAAAGGACAGTTGTGCTCTGCCACAAACAGGCCTTCCCT  
TCTACCACCAACTACTGCCCTTAAGGTTCTTGTGGTTTACCATCTGAAATATGTTCCA  
TCACACAATTGTTACTTCACTGAATTCTCAAAACCATTGCAGAAGTGAGGTATCCTTGAA  
AGTGGCAGAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTGCCACTCAAAGAGCA  
GCAGACAAAGTCGCTTCCCTTCCAATGACGTCAACAGTGTGCGATGGTACCTGTGGCAA  
GAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTTCCCCCTGCCCTTAACCTTGCA  
GTGATCTAAGAACGCCAGATTCTGACAAATACGTGGTGTACTTAGAGAGATTGATACA  
AAAGACGATTACAATGCTCTCAGTGTCTGCCCAAGTACCACTCATGAAGGATGCCACTGCTT  
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAGATCACAAAGCCTGCCACG  
ATGGCTGCTGCCCTG**TAG**

## **FIGURE 158**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRDLRVEPVITSVATGDYSILMNWSVL  
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP  
NANMNEGPGSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKNEETVEVNFTTTPLGNRYMALIQH  
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPQTGVPFPLDNNK  
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTLLPPIKVLIVVYPSEICFHHTICYFTEFL  
QNHCRCSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA  
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVQQVSAGKRSQACHD  
GCCSL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**Transmembrane domain:**

amino acids 290-309

**N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283  
- 287

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

**Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

**N-myristoylation site.**

amino acids 116-122

**Amidation site.**

amino acids 488-452

## **FIGURE 159**

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAGTACTTGCTGCT  
GTCGATATTGGGGCTTGCCTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA  
CTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC  
ATCATCAATGAAAACCAGCGCGTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG  
GAATTACACTGTCACTTGGGACCCAACCGTACCCCTCGGAAGTTGTACAGGCCAGTGTAGGA  
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCATCCAGCAA  
GAGACCCTGGTCGTCGGAGGAAGCACCAAGGCTGCTCTGTTCTTCCAGTTGGAGAAGGTGCT  
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTAAGAGGTGCATATCC  
ACTCAGCTGAAGAAG

## **FIGURE 160**

MTVKTLHGPAMVKYLLSILGLAFLSEAAARKIPKVGHFFQKPESCPVPGGSMKLDIGIINEN  
QRVSMSRNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRLGCINAQGKEDISMNSVPIQQETLVV  
RRKHQGCSVSFQLEKVLVTVGCTCVTPVIHHVQ

**Signal sequence:**

amino acids 1-30

**N-glycosylation site.**

amino acids 83-87

**N-myristoylation sites.**

amino acids 106-111, 136-141

## **FIGURE 161**

ACACTGGCAAACAAAAACGAAAGCACTCCGTCTGGAAGTAGGAGGAGTCAGGACTCCCAGG  
ACAGAGAGTGCACAAACTACCCAGCACAGCCCCCTCCGCCCTCTGGAGGCTGAAGAGGGATTC  
CAGCCCCCTGCCACCCACAGACACAGGCTGACTGGGTGCTGCCCTCTGGGGGGGGCAGCAC  
AGGGCCTCAGGCCTGGTGCCACCTGGCACCTAGAAGATGCTGTGCCCTGGTTCTGCTGTCT  
TGGCACTGGGCCAGGCCAGTGGCTTCTCTGGAGAGGCTTGTTGGGCCCTCAGGACGCTACC  
CACTGCTCTCCGGGCTCTCCGCGCTCTGGGACAGTGACATACTCTGCCTGCCCTGGGACAT  
CGTGCCTGCTCCGGCCCCGTGCTGGGCCCTACGCACCTGCAGACAGAGCTGGTGCTGAGGTGCC  
AGAAGGAGACCGACTGTGACCTCTGTCTCGGTGTTGCACTTGGCGTGCATGGGACTGG  
GAAGAGCCTGAAGATGAGGAAAAGTTGGAGGAGCAGCTGACTCAGGGTGGAGGAGCCTAGGAA  
TGCCTCTCCAGGCCAAGTCGTCTCTCCAGGCCAACCTACTGCCGCTGCGTCTGC  
TGGAGGTGCAAGTGCCTGCTGCCCTTGTCAGTTGGTCAGTCTGTTGGCTCTGTTATATGAC  
TGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGTCCTATAACTCAGGCCAGGTACGAGAA  
GGAACATCAACCACACACAGCAGTCGCTGCCCTGGCTAACGTGTCAGCAGATGGTGACA  
ACGTGCATCTGGTTCTGAATGTCCTGAGGAGCAGCATTGGCCTCTCCCTGTA  
CTGGGAATCAG  
GTCCAGGGCCCCAAAACCCGGTGGCACAAAAACCTGACTGGACCGCAGATCATTACCTTGA  
CCACACAGACCTGGTCCCTGCTGTATTCAAGGTGTCGCTCTGGAACCTGACTCCGTTAGGA  
CGAACATCTGCCCTTCAGGGAGGACCCCCCGCAGACACCAGAACCTCTGGCAAGCCGCCGACTG  
CGACTGCTGACCCCTGAGAGCTGGCTGCTGGACGCCACCGTCTCGCTGCCGAGAACGGGCA  
CTGCTGGGGCTCCGGTGGGACCCCTGCCAGCCACTGGTCCCACCGCTTCTGGAGAACG  
TCACTGTGGACAAGTTCTCGAGTCCCATTGCTGAAAGGCCACCTAACCTCTGTTAGGTG  
AACAGCTGGAGAACGCTGCAAGCTGAGGAGTGCTGTGGCTGACTCCCTGGGCCCTCTCAAAGA  
CGATGTGCTACTGTGGAGAACGAGGCCAGGACACAGATCCCTGTCCTTGA  
CTGGCTGACTTCACTACCCAGAAAGCCTCACAGGGCAGCTGCCCTGGAGAGTACTTACTA  
CAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGAGCCTATGGCCTG  
CCCCATGGACAAATACATCCACAAGCGCTGGCCCTGCTGTGGCTGCCCTACTCTTGGC  
CTGCGCTTCCCTCATCCTCTCTCAAAAAGGATCACCGCAAAGGGTGGCTGAGGCTTGTAAA  
CAGGACGTCCGCTGGGGCGGGCGCAGGGCCGCGCGCTCTGCTCCCTACTCAGCGATGA  
CTCGGGTTTCGAGGCCCTGGTGGCGCCCTGGCGTGGCCCTGTGCCAGCTGCCGCTGCGCTGG  
CCGTAGACCTGTGGAGGCCGTCGTAAGTGAAGCGCGCAGGGGCCGTTGGCTTACCGCAG  
CGGCAGACCCCTGCAAGGAGGGCGCGTGGTGGCTTGTCTTCTCTCCGGTGGCTGGGCG  
GTGCAGCGAGTGGCTACAGGATGGGTGTCGGGCCGGCGCAGGCCCGCACGACGCCCTCC  
GCGCCTCGCTCAGCTGCGTGCTGCCGACTTCTGCAAGGCCGGCGCCGGCAGCTACGTGGGG  
GCCCTGCTTCGACAGGCTGCTCCACCGGACGCCGTACCCGCCCTTCCGCACCGTGCCGCTT  
CACACTGCCCTCCCAACTGCCAGACTTCTGGGGCCCTGCAGCAGCCTCGCGCCCCCGTCC  
GGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCGGGCCCTCAGCAGCCCTGGATAGCTACTTC  
CATCCCCGGGACTCCCGCAGGGACGCGGGTGGGACCGAGGGCGGGACCTGGGGGGGG  
CGGGACTTTAAATAAAGGCAAGCGCTGTTTCTAAAAAAA

## **FIGURE 162**

MPVPWFLLSLALGRSPVVLSLERLVPQDATHCSPGLSCRILWSDILCLPGDIVPAPGPVLAPTHLQTELVL  
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLFSQAYPTARCVLLEV  
QVPAALVQFGQSVGSVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVS  
EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLPCLCIQVWPLEPDVRTNICPFREDPRAHQN  
LWQAARLRLTLQSWLLDAPCSLPAEAALCWRAPIGGDPQCPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ  
VNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSILCALEPSGCTSLEPKASTRAARLGEYLLQDLQS  
GQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLLLLKKDHAKGWLRLLKQDVRSAGAAARG  
RAALLLYSADDGFERLVGALASALCQLPLRVAVDLWSRRELQAQGPVAWFHAQRQTLQEGGVVLLFSP  
GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFT  
LPSQLPDFL GALQQPAPRSGRLQERAEQVSRALQPALDSYFHPPGT PAPGRGVGPAGPGAGDGT

**Signal sequence:**

amino acids 1-20

**Transmembrane domain.**

amino acids 453-475

**N-glycosylation sites.**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,  
334-337, 357-360, 391-394

**Glycosaminoglycan attachment site.**

amino acids 583-586

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 552-555

**N-myristoylation sites.**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,  
692-697, 696-701, 700-705

## **FIGURE 163**

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTGACTGTGGATCCCTGGCT  
GCTCACGCCCCCTGAGGGACCCCTCGATCTGCTCCAGCACGTGAAATTCCAGTCCAGCAACTTTGA  
AAACATCCTGACGTGGGACAGCGGGCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA  
AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTCAGCGATCACCCGAAAGTCCTGC  
AACCTGACGGTGGAGACGGCAACCTCACGGAGCTACTATGCCAGGGTCACCGCT  
GTCAGTGCAGGGAGGGCGGTCAGGCCACCAAGATGACTGACAGGTTAGCTCTGCAGCACACTAC  
CCTCAAGCCACCTGATGTGACCTGTATCTCAAAGTGAGATGATTAGCTCATCCTA  
CCCCCAGCCAATCCGTGCAGGGATGGCCACCGGCTAACCCCTGGAAGACATCTCCATGACCTG  
TTCTACCAACTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTGGAGGGAAAGCAGAGAGA  
ATATGAGTTCTCGGCCCTGACCCCTGACACAGAGTTCCCTGGCACCATCATGATTGCGTTCCA  
CCTGGCCAAGGAGAGTGCCCCCTACATGTGCCAGTGAAAGACACTGCCAGACGGGACATGGACC  
TACTCCTCTCCGGAGCCTCCCTGTTCTCATGGGCTTCTCGTCGAGTACTGCTACCTGAG  
CTACAGATATGTCACCAAGCCGCTGCACCTCCAACTCCCTGAACGTCCAGCGAGTCCGTACTT  
TCCAGCCGCTGCCTCATCCAGGAGCACGCTCTGATCCCTGTTGACCTCAGCGGCCCCAGC  
AGTCTGGCCCAGCCTGTCAGTACTCCAGATCAGGGTGTCTGGACCAGGGAGCCGAGGAGC  
TCCACAGCGGCATAGCCTGTCCAGATCACCTACTTAGGGCAGCCAGACATCTCCATCCAGC  
CCTCAAACGTGCCACCTCCCCAGATCCTCTCCCTGCTCTATGCCCTAACGCTGCCCCCTGAG  
GTCGGGCCCCCATCTTATGCACCTCAGGTGACCCCGAAGCTCAATTCCCATCTACGCCCCACA  
GGCCATCTCAAGGCCAGCCTCTCTATGCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT  
CCTATGGGTATGCATGGAAAGGTCTGGCAAAGACTCCCCACTGGACACTTTCTAGTCCTAAA  
CACCTTAGGGTCAAAGGTCAGCTTCAGAAAGAGCCACCAAGCTGGAAAGCTGCATGTTAGGTGGCCT  
TTCTCTGCAGGAGGTGACCTCTGGCTATGGAGGAATCCAAGAAGCAAATCATTGCACCAAGC  
CCCTGGGATTGCAAGACAGAACATCTGACCCAAATGTGCTACACAGTGGGAGGAAGGGACA  
CCACAGTACCTAAAGGCCAGCTCCCCCTCCTCTCAGTCCAGATGAGGGCACCCCATGTC  
CCTCCCTTGCAACCTCCTCCGGTCCATGTTCCCCCTGGACCAAGGTCCAAGTCCCTGGGCC  
TGCTGGAGTCCCTTGCTGTGCTCCAGGATGAAGCCAAGAGCCAGCCCCCTGAGACCTCAGACCTG  
GAGCAGCCCACAGAACCTGGATTCTTCAAGAGCCTGGCCCTGACTGTGCA  
GAGTGGGAGTCTG  
AGGGAAATGGGAAAGGCTTGGTCTTCCCTGTCCTACCCAGTGT  
CACATCCTGGCTGTCA  
ATCCCCATGCCTGCCATGCCACACTCTGGCATCTGGCTCAGACGGGTGCCCTGAGAGAAC  
AGAGGGAGTGGCATGCAGGGCCCTGCCATGGGTGCGCTCCTCACCGGAACAAAGCAGCATGATA  
AGGACTGCAGGGGGAGCTCTGGGGAGCAGCTTGTAGACAAGCCGTGCTGGCTGAGCCCTG  
CAAGGCAGAAATGACAGTGCAAGGAGGAATGCAGGGAAACTCCCGAGGTCCAGAGCCCCACCTC  
CTAACACCATGGATTCAAAGTGCTCAGGGAAATTGCTCTCCTTGCCCCATTCTGGCCAGTTTC  
ACAATCTAGCTCGACAGAGCATGAGGCCCTGCCCTTCTGTGATTGTCAAAGGTGGGAAGAGA  
GCCTGGAAAAGAACCAAGGCCAGGGAAAGAACCAAGAGGAGGCTGGCAGAACAGAACAC  
ACTTCTGCCAAGGCCAGGGCAGCAGGACGCGAGACTCTAGGGAGGGTGTGGCTGCAGCTCA  
TTCCCAGCCAGGGCAACTGCCAGCTGACGTTGCACTGATTCAGCTCATTCCTGATAGAACAAAGC  
GAAATGCAGGTCCACCAAGGGAGGGAGACACACAAGCCTTCTGAGGCAGGAGTTCAAGACCC  
ATCCCTGAGAATGGGGTTGAAAGGAAGGTGAGGGCTGIGGCCCTGACGGGTACAATAACAC  
TGTACTGATGTCACAACCTTGCAAGCTCTGCCCTGGGTTCAAGCCCATCTGGGCTCAAATTCCAGC  
CTCACCAACTCACAAGCTGTGACTCAAACAAATGAAATCAGTGCCAGAACCTCGGTTCTC  
ATCTGTAATGTGGGATCATAACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG  
TCTTTAAAGTGCTTAATAGTGCCCTGGTACATGGCAGTGCCCAATAACGGTAGCTATTTAAAAA  
AAAAAAAA

## **FIGURE 164**

MRTLLTILTGVSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW  
VAKKGCQRITRKSCNLTVEGNLTELYYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVT CIS  
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHLGGKQREYEFFGLTPDT  
EFLGTIMICVPTWAKESAPYMCRVKTLPDRWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP  
PNSLNQVRVLTFQPLRFIQEHVLIPIVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT  
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFPFYAPQAISKVQPSSY  
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPPAGSCMLGGLSLQEVTSLAM  
EESQEAKSLHQPLGICTDRTSDPNVLHSGEEGTPQYLKGQLPLLSSVQIEGHPMSLPLQPPSGPC  
SPSDQGPSPWGLLESVCPKDEAKSPAPETSDLEQPTELDSLFRGLALTQWES

**Signal sequence.**

amino acids 1-17

**Transmembrane domain.**

amino acids 233-250

**N-glycosylation sites.**

amino acids 80-83, 87-90, 172-175

**N-myristoylation sites.**

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

## **FIGURE 165**

TGGCCTACTGGAAAAAAAAAAAAAAAGTCACCCGGGCCCGCGTGGCCACAACATGG  
CTGCGGCCGGGCTGCTCTCTGGCTGTCGTGCTGGGGCGCTCTGGTGGTCCCAGGCCAG  
TCGGATCTCAGCCACGGACGGCGTTCTGACCTCAAAGTGTGCAGGGACGAAGAGTGCAGCAT  
GTTAATGTACCGTGGAAAGCTCTTGAAAGACTTCACGGCCCTGATTGCGTTTGAAATTAA  
AAAAAGGTGACGATGTATATGTCTACTACAAACTGGCAGGGGATCCCTGAACCTTGGCTGGA  
AGTGTGAACACAGTTGGATATTTCAAAAGATTGATCAAGGTACTTCATAAAACACGGA  
AGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGCTGCTTGAAGGAGGAAGAGATGATT  
TTAATAGTTATAATGTAGAAGAGCTTTAGGATCTTGAACTGGAGGACTCTGTACCTGAAGAG  
TCGAAGAAAGCTGAAGAAGTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTGGGGCGTGA  
ACTTGACCCCTGTGCCTGAGCCCCAGGCATTCAAGAGCTGATTCAAGAGGATGGAGAAGGTGCTTCT  
CAGAGAGCACCAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCACACCAGCGGT  
CCTGCAGCTAACGCTCAGGGAGTGCAGTCTCGTTGGACACTTGAAGAAATTCTGCACGATAA  
ATTGAAAGTGCCGGAAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTGGAGCAGGGAGA  
AGACAGATGCTTACAAAGTCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTTATT  
CATTACAGCAAAGGATTCGTTGGCATAAAATCTAAGTTGTTTACAAAGATTGTTTTAGTA  
CTAAGCTGCCTTGGCAGTTGCATTTGAGCCAACAAAATATTATTTCCCTTAAGTA  
AAAAAAAAAAAAAA

## **FIGURE 166**

MAAAPGLLFWLFWLGA LWVWVPGQSDLSHGRRFSDLKVC GDEEC SMLMYRGKALEDFTGPDCRFVN  
FKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADETDFVC FEGGRD  
DFNSYNVEELLGSLELEDSPVEESKKAAEVSQHREKSPPEESRGRELDPVPEPEAFRADSEDEGA  
FSESTEGLQGQPSAQESHPHTSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER  
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYKDCF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 294-298

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34

**Tyrosine kinase phosphorylation site.**

amino acids 67-76

**N-myristoylation sites.**

amino acids 205-211, 225-231, 277-283

**Amidation site.**

amino acids 28-32

## **FIGURE 167**

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAAGAGGCCGGGAAGAGAAGCAAAGCGC  
AACGGTGTGGTCCAAGCCGGGCTTCGCTCGCCTCTAGGACATAACACGGGACCCCCTAACCTTC  
AGTCCCCAAACGCGCACCTCGAAGTCTTGAACTCCAGCCCCGCACATCCACGCGCGGCACAGG  
CGCGGCAGGCAGGCGCAGGTCGGCGAAGGCAGTCGCGCAGGGGTCGGGCAGCTGGGCTGGG  
GGCAGGGAGTAGGGCCCGCAGGGAGGCAGGGAGGCTGCATATTCAAGAGTCGCGGCTGCGCCCTG  
GGCAGAGGCCGCCCTCGCTCACGCAACACCTGCTGCTGCCACCGCGCCGCGATGAGCCGCGTGG  
TCTCGCTGCTGCTGGCGCCGCGTGCCTGCGGCCACGGAGCCTCTGCCGCCGCGTGGTCAGC  
GCCAAAAGGTGTGTTTGCTGACTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAAC  
GTCCAGCCGAGTGAAGCTTCAGGAGGCACGCCTGGCTGTGAGAGTGAGGGAGGAGTCCTCCTCA  
GCCTTGAGAATGAAGCAGAACAGAACAGTAATAGAGAGCATGTTGAAAACCTGACAAAACCCGG  
ACAGGGATTCTGATGGTATTCTGGATAGGGCTTGAGGAATGGAGATGGCAAACATCTGG  
TGCCTGCCAGATCTTACCAAGTGGCTGATGGAAGCAATTCCCAGTACGAAACTGGTACACAG  
ATGAACCTCCTGCGGAAGTGAAGAAAGTGTGTTGATGTATCACCAACCAACTGCCAACCTGGC  
CTTGGGGGTCCTACCTTACCAAGTGGATGATGACAGGTGTAACATGAAGCACAATTATATTG  
CAAGTATGAACCAGAGATTAATCCAACAGCCCTGAGAAAAGCCTTATCTTACAAATCAACCAG  
GAGACACCCATCAGAATGTGTTACTGAAGCAGGTATAATTCCAATCTAATTATGTTGTT  
ATACCAACAATACCCCTGCTTACTGATACTGGTTGCTTTGGAACCTGTTGTTCCAGATGCT  
GCATAAAAGTAAAGGAAGAACAAAAACTAGTCAAACACCAGTCTACACTGTGGATTCAAAGAGTA  
CCAGAAAAGAAAGTGGCATGGAAGTATAAAACTCATGACTGGTTCCAGAATTGTAATTCT  
GGATCTGTATAAGGAATGGCATCAGAACAAATAGCTTGGGAATGGCTGAAATCACAAGGATCTGC  
AAGATGAACTGTAAGCTCCCTTGAGGCAAATTAAAGTAATTGTTATATGTCTATTATTCA  
TTTAAAGAATATGCTGTGCTAATAATGGAGTGAACATGCTTATTTGCTAAAGGATGCCACCAA  
ACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTGTATCAACACGTGGGAGTA  
TGTGTGTTAGAAGCAATTCTTTATTCTTACCTTCATAAGTGTATCTAGTCAATGTA  
TGTATATTGTTGAAATTACAGTGTGCAAAGTATTACCTTGCATAAGTGTGTTGATAAAA  
ATGAACCTGTTCTAATATTATTATGGCATCTCATTTCAATACATGCTTTGATTAAAG  
AAACTTATTACTGTTGTCACGTGAATTCACACACACAAATATAGTACCATAGAAAAGTTGT  
TTCTCGAAATAATTCAATTGTCAGCTCTGCTTGGTCAATGTCTAGGAAATCTTCAGA  
ATAAGAAGCTATTCAATTGTCAGCTTGTGAAACACTATGCAATTGAAACAAAAGAAG  
TGTCTAATTCAATTGTCAGCTTGTGAAACACTATGCAATTGCAATTGAAACAAAAGAAG  
TGACATACACAATATAAATCATATGCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTGA  
GGGTTCTGAAATCAATGTGGCCCTCTTGCCCACTAAACAAAGATGGTTGTTGGGGTTGG  
ATTGACACTGGAGGCAGATAGTGCAGGAAAGTGTCTAAGGTTCCCTAGCTGTATTAAGCCTCTG  
ACTATATTAGTATAAAAGAGGTATGTGGTTGAGACCAGGTGAATAGTCACATCAGTGTGGAG  
ACAAGCACAGCACACAGACATTAGGAAGGAAAGGAACATCGAAATCGTGTGAAAATGGGTGG  
AACCCATCAGTGCATATTCAATTGATGAGGGTTGCTTGAGATAGAAAATGGTGGCTCCTT  
CTGCTTATCTCTAGTTCTCAATGCTTACGCCCTGTTAACCAAATAAAGAGTTCTGTTCTGGGGAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 168**

MSRVVSLLGALLCGHGFCCR VVSGQKVC FADF KHP CYK MAYF H E LSS RVS F QEAR LACE SE  
GGVLLSLENEAEQKLIESMLQNLTKPGTG ISDGDFWIGLWRNGDQTSGACP DLYQ WSDGSNSQ  
YRNWYTDEPSCGSEKCVV MYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAPVEK  
PYLTNQP GDTHQN VVVTEAGIIPNLI YVVIPTIPLLLLILVAFGTCCFQMLHKS KGRTKTSPNQ  
STLWISKSTRKESGM EV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89, 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217